

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 25, 2003, 08:48:53 ; Search time 2746 Seconds
(without alignments)
10958.595 Million cell updates/sec

Title: US-09-955-526-3
Perfect score: 1034
Sequence: 1 gagcaacataacattgtct.....ataaggaagttccttctgtga 1034

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_ss.*
28: em_un.*
29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rod.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB	ID	Description
1	52.7	545	1293	8	AF390556	AF390556 Nicotiana
2	42.8	41.5	1066	8	AY087532	AY087532 Arabidops
3	42.7	41.3	994	8	AY091134	AY091134 Arabidops
4	42.7	41.3	1005	8	AF208124	AF208124 Arabidops
5	42.7	41.3	1117	8	AB025927	AB025927 Arabidops
6	42.0	40.6	775	8	AY114059	AY114059 Arabidops
7	41.8	40.4	1010	8	AF390555	AF390555 Brassica
8	41.3	40.0	1013	8	AF433320	AF433320 Brassica
9	39.2	38.6	1019	8	AF453321	AF453321 Brassica
10	35.1	33.9	1181	8	AB025926	AB025926 Oryza sat
11	34.5	33.4	744	8	HVU290421	AJ290421 Hordeum v
12	178.6	17.3	418	11	G73645	G73645 RZ957F etio
13	137.2	13.3	360	11	G71526	G71526 Ag1521534FM
14	125.2	12.1	892	9	AF033095	AF033095 Homo sapi
15	125.2	12.1	2609	9	BC000916	BC000916 Homo sapi
16	122.8	11.9	1745	5	AF220548	AF220548 Paralicit
17	122	11.8	2600	9	HSTEGT	X75861 H.sapiens T
18	122	11.8	2634	6	AR058920	AR058920 Sequence
19	122	11.8	2634	6	AR058921	AR058921 Sequence
20	122	11.8	2634	6	AR112791	AR112791 Sequence
21	122	11.8	2634	6	AR112792	AR112792 Sequence
22	119.8	11.6	2331	10	BC005588	BC005588 Mus muscu
23	113.8	11.0	3498	8	AB025609	AB025609 Arabidops
24	108.4	10.5	896	10	RNTEGT3	X75856 R.norvegicu
25	98.4	10.5	940	10	RNTEGT2	X75855 R.norvegicu
26	94.6	9.1	127507	2	AF005311	AF005311 Oryza sat
27	94.6	9.1	155492	2	AF005304	AF005304 Oryza sat
28	87.4	8.5	198788	8	ATCHRIV46	AL161546 Arabidops
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35	46	4.4	5100	9	AF084196	AF084196 Pan trogl
36	46	4.4	7436	9	AF061786	AF061786 Homo sapi
37	46	4.4	72871	2	AC091550	AC091550 Homo sapi
38	46	4.4	108122	2	AC116905	AC116905 Homo sapi
39	46	4.4	153077	9	AC020679	AC020679 Homo sapi
40	46	4.4	170558	2	AC012414	AC012414 Homo sapi
41	46	4.4	184108	2	AC023191	AC023191 Homo sapi
42	46	4.4	211391	2	AC037471	AC037471 Homo sapi
43	45.2	4.4	6849	2	AC118646	AC118646 Mus muscu
44	45.2	4.4	6849	2	AC118646	AC118646 Mus muscu
45	45.2	4.4	68931	2	AC117831	AC117831 Mus muscu

ALIGNMENTS

RESULT 1
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LOCUS AF390556 1293 bp mRNA linear PLN 16-JUL-2001
DEFINITION Nicotiana tabacum Bax inhibitor 1 (BI-1) mRNA, complete cds.
ACCESSION AF390556
VERSION AF390556.1 GI:14719275
KEYWORDS
SOURCE Nicotiana tabacum.
ORGANISM Nicotiana tabacum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
REFERENCE
1 (bases 1 to 1293)
AUTHORS Bolduc,N., Pitre,F. and Brisson,L.
TITLE Characterization of Bax inhibitor 1 from Nicotiana tabacum

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1293)
AUTHORS Bolduc, N., Pitre, F. and Brisson, L.
TITLE Direct Submission
JOURNAL Submitted (11-JUN-2001) Biochemistry and Microbiology, Laval University, Quebec G1K 7P4, Canada
FEATURES
Location/Qualifiers
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/cultivar="SR-1"
/db_xref="taxon:4097"
/tissue type="leaf"
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/gene="BI-1"
CDS 134..883
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LFWLHFASSIFGSMALFKFEYVGLVFGYIFDIQIIIEAKHGLDLDIVKHALTI
FTDFVAVFVIRILLIMLNKNSDKKKKRN"
BASE COUNT 296 a 243 c 304 g 450 t
ORIGIN
Query Match 52.78; Score 545; DB 8; Length 1293;
Best Local Similarity 83.28; Pred No. 1.5e-134;
Matches 633; Conservative 0; Mismatches 125; Indels 3; Gaps 1;
QY 75 AAGAAGAGAACATGGAAGTTTCACATCGTTCTTCGACTCGCAATCTG---CCTCTCGC 131
DB 122 AAGAAGAGAGAAATGGAGCTTGGACATCGTTCTTCAATTCACATCGCGGCTGCTCGC 181
QY 132 AACCGCTGAGTATGATTCTCAAAACATCCGACAGATCTCACCTCTCGTTCAAAC 191
DB 182 ATCTCTGAGTTAGCATCTTCTTAAGAACTTCGCGAGATCTCTCCCTTGTTCAACT 241
QY 192 CATCTCAAGCAGTGTACTTACGCTATCTGTCTTGTAGTGGCATCGCTGTGGGCT 251
DB 242 CATCTCAAAAGGCTACCTTTTCAATATGTTGTCTTGTAGTGTCTCGGCTGTGGAGCT 301
QY 252 TACCTTCACATCTATGAATATCGTGGCTCTCTCACAAATGGCTTCAGTGGAGC 311
DB 302 TACCTTCACATCTTTGGAACATATGGTGGCTTACTTACGACATGGAGATGGAGAGC 351
QY 312 ATGGTGTGCTTCTCTAGCTCTCTTATCAAGAGCAAAAGGGTGGCTCTTCTGATG 371
DB 362 ATAGTGTGCTGATGGCAGACCTCTGTATGAGAGCAAAAGAGATAGCACATCTGATG 421
QY 372 GCAGCTGCATTTTGAAGGCGCTCTATTGCTCTCTGATGAGCTGGGCATTAATCTC 431
DB 422 GCAGCTGCATCTTTAAGAGAGCATCTATTGGTCCACTGATGATGAAATGGCTATGACT 481
QY 432 GATCCAAGCATTTGTTTGGCGCTTTTGTAGGTTGTGCTGTGTTTGGTGTCTCTCA 491
DB 482 GACCCAAGCATTTGATCGGTCTTTTGTGGTGTGCTGTGGCTTTGTTGTTCTCA 541
QY 492 GCTGTGCTCATCTTGGCAGGCGAGGAGTACTTACTTCGGGCGCTTCTTCACT 551
DB 542 GCTGTGCTCATCTTGGCAGGCGAGGAGTACTTATCTTTGGAGCTCTCTTCACT 601
QY 552 GGCGTCTCCCTTCTCTTGTGTGACCTTTGATCCTCCATTTTGGTGGTTCATGGCT 611
DB 602 GGTCTCTCATCTTTTGTGGTGTGACCTTCGCTCCCTCCATTTTGGTGGTTCATGGCC 661
QY 612 GTTTCAGTTTGTGTTATTTGGACTCTTGGTGTGTTTGGGCTACATCGCTTGTGAC 671
DB 662 TTGTTCAAGTTCAGGTTTATTTGGGCTCTTGGGCTTGTGGGCTATATCATTTTGC 721
QY 672 ACCCAAGAAATTAATGAGAAGGCTCACTTGGGTGATATGATTAAGATGATGATTC 731

Db 722 ACCAAGATATAATTGAGAAGGCACACCTTGGGATTTGGACTACGTGAAGCATCTCTG 781
QY 732 ACCCTTTTCACAGATTTCGCGCTGTTTTCGCGGANTTCTGATCATCATGTTAAGAAAT 791
Db 782 ACCCTCTTTACAGATTTCGCTGTTTTCGCGAATATTATCATATAATGCTGAAGAT 841
QY 792 GCATCTGAGAGGAAG 832
Db 842 GCATCCGACAGGAG 882
RESULT 2
AY087532 1066 bp mRNA linear PLN 26-JUN-2002
LOCUS Arabidopsis thaliana clone 36400 mRNA, complete sequence.
DEFINITION Arabidopsis thaliana
ACCESSION AY087532
VERSION AY087532.1 GI:21406269
KEYWORDS FLI CDNA.
SOURCE
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 1066)
Haas,B.J., Volfovsky,N., Town,C.D., Trukhan,M., Alexandrov,N.,
Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.
Full-length messenger RNA sequences greatly improve genome
annotation
Genome Biol. (2002) In press
2 (bases 1 to 1066)
Brover,V., Trukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
Feldmann,K.
Full-length cDNA from Arabidopsis thaliana
Unpublished
3 (bases 1 to 1066)
Brover,V., Trukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
Feldmann,K.
Direct Submission
Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
Malibu, CA 90265, USA
This clone sequence is one of 5,000 Ceres full-length cDNAs made
available to TIGR and Genbank. The following quality assessment of
this set was done by comparison with known proteins: two percent of
the clones are estimated to be 5'-truncated; less than one percent
are 3'-truncated; approximately two percent represent alternative
splice variants, including unspliced introns and spliced exons; one
percent may contain premature stop codons; five percent may have
frame shifts in a coding region. A sequence is considered to be
5'-truncated if it lacks the translation initiation start (ATG). A
sequence is considered to be 3'-truncated if it lacks the
C-terminal end of the encoded protein. Please note that these cDNA
sequences are derived from the Ws or Laer ecotypes and therefore
may contain polymorphisms when compared to sequences from Col-0.
Genet carried out the library production and sequencing of the
full-length clones. Ceres, Inc. carried out the clustering of the
5' sequences, selection of clones, and sequence assembly.
FEATURES
source 1..1066
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BASE COUNT 268 a 205 c 224 g 369 t

ORIGIN

Query Match 41.5%; Score 428.8; DB 8; Length 1066;
Best Local Similarity 73.7%; Pred. No. 1.6e-103;
Matches 560; Conservative 0; Mismatches 137; Indels 3; Gaps 1;

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2Y 72 AAGAGAAGAGAACAAATGAAGGTTTCAATGTTCTTCGACTCGAATCTCGCTCTCGC 131
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Db 34 AAAAAAAGAGAAACAAATGATGCGTTCTTCTCTTTCGATTCTCAACCTG---GTAGC 90
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2Y 132 AACCGCTGGAGTTATGATTCTCTCAAAACATTCGCCAGATCTCACCTCTCGTTCAAACT 191
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Db 91 AGAAGCTGGAGCTATGATTCTCTTAAACATTCCTCGATTTCTCAGCGGTTCAAGAT 150
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2Y 192 CATCTCAAGACAGGTACCTTACGTTATGCTGTCTTATGAGGATCGCTGCTGGGCT 251
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Db 151 CATCTTAAACGGGTTTATTTGACCTTATGCTGTCTTGTGGGCTCTGCTTTGGAGCT 210
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2Y 252 TACCTTCACATTTCTATGGAATATCGGTGCGCTTCACAAAGATGGCTTGCATGGGAGC 311
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Db 211 TACCTCCATGTGCTCTGGAATATCGCGGTATCTTACACGATGGATGTTTGGAACT 270
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2Y 312 ATGGTGTGGCTTCTCTCAGCTCTCTCTTATCAAGACGAAAAAGGTTGCTTCTCTGATG 371
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Db 271 ATGATTTGGCTCTCTCTCATGCTCTCTTATGAACACCAAAAAAGGCTTCTCTCTGTT 330
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2Y 372 GCAGCTGCACCTTTTGAAGCGCCCTATTTGGTCTCTGATTGAGCTGGGCATTAACCTC 431
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Db 331 GCGTCTGCTGTTCTTGAAGGTGCTTCTGTGTGCGCTTGTATCAAGTGGCAATGATGTT 390
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2Y 432 GATCCAGCAATGTGTTTGGCGCTTTTGTAGTGTGCTGTGTTTTTGGTGTCTTCTCA 491
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Db 391 GACCAAGCATCTTATCATCTGCTGTTTGTGGAATCGCATAGCGTTTGTCTGTCTTCTCA 450
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2Y 492 GCTGCTGCATGTTGCAAGGCGCAGGAGTACTTGTACCTCGGGGCTTCTTCTCATCT 551
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Db 451 GCAGCAGCAATGTACGACAGCGAGGAGTATCTACTCTTGGAGGACTGCTTTCATCT 510
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2Y 552 GCGGTCTCCCTTCTCTTCTGCTTGTGCACTTGTGATCTTCTCATTTTGTGTTTCCATGCT 611
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2Y 612 GTTTTCAAGTTGAGTTGATTTTGGACTCTTGTGTTTGTGGGCTCATGCTCTTTGAC 671
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2Y 792 GCATCTCAGAGGAAGAGAGAGAGAGAGAGAGAGAGAACT 831
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Db 751 TCAGCAGATAAGAGAGAGAGAGAGAGAGAGAGAGAACT 790
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RESULT 3

AY091134 994 bp mRNA linear PLN 22-APR-2002
LOCUS Arabidopsis thaliana putative Bax inhibitor-1 (At5g47120) mRNA,
complete cds.
DEFINITION AY091134.1 GI:20268759
VERSION AY091134.1
KEYWORDS FLI CDNA.
SOURCE Arabidopsis thaliana.
ORGANISM Arabidopsis thaliana.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi-
s
REFERENCE 1 (bases 1 to 994)

AUTHORS

Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M.,
Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L.,
Tang, C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L.,
Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,
Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,
Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J.,
Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A.,
Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.

TITLE

JOURNAL

REFERENCE

AUTHORS

2 (bases 1 to 994)
Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M.,
Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L.,
Tang, C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L.,
Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,
Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,
Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J.,
Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A.,
Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
Direct Submission
Submitted (20-MAR-2002) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL CDNA : 'RIKEN
Arabidopsis Full-Length cDNA'): Seki, M., Narusaka, M., Ishida, J.,
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
Hayashizaki, Y. and Shinozaki, K.

TITLE

JOURNAL

COMMENT

The Salk, Stanford, PGE (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs: Yamada, K., Banh, J.,
Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M.,
Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C.,
Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Chen, H.,
Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J.,
Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P.,
Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.

Yamada, K. (SSP/PGE) and Seki, M. (RIKEN GSC) contributed equally to
this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGE)
contributed equally to this work as PIs.

FEATURES

Source

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BASE COUNT

ORIGIN

256 a 194 c 209 g 335 t

REFERENCE
1 (bases 1 to 1006)
Koski; eurosil II; brassicales; brassicaceae; microphytes.

AUTHORS
Sanchez, P., de Torres Zabala, M. and Grant, M.
AtBI-1, a plant homolog of Bax inhibitor 1, suppresses Bax-induced
cell death in yeast and is rapidly upregulated during wounding


```

QY 672 ACCAAGAAATTATTGAGAGGCTCACTTGGGTGATATGGATTACGTTAAGCATGCAATTG 731
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Db 748 TCAGCAGATAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 787

RESULT 5
AB025927 1117 bp mRNA linear PLN 04-MAR-2000
LOCUS Arabidopsis thaliana AtBI-1 mRNA for Bax inhibitor-1, complete cds.
DEFINITION Arabidopsis thaliana (strain:Columbia) cDNA to mRNA.
ACCESSION AB025927
VERSION AB025927.2 GI:7209773
KEYWORDS Bax inhibitor-1.
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana (strain:Columbia) cDNA to mRNA.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (sites)
REFERENCE Kawai, M., Pan, L., Reed, J.C. and Uchimiya, H.
AUTHORS Evolutionally conserved plant homologue of the Bax inhibitor-1
TITLE (BI-1) gene capable of suppressing Bax-induced cell death in
yeast (1)
JOURNAL FEBS Lett. 464 (3), 143-147 (1999)
MEDLINE 20086876
REFERENCE 2 (bases 1 to 1117)
AUTHORS Kawai, M. and Uchimiya, H.
TITLE Direct Submission
JOURNAL Submitted (06-APR-1999) Hirofumi Uchimiya, University of Tokyo,
Inst. Mol. Cellu. Biosci., Cellular Function; 1-1-1 Yayoi,
Bunkyo-ku, Tokyo 113-0032, Japan
[B-mail:uchimiya@imcbns.iam.u-tokyo.ac.jp, Tel:81-3-3812-2910,
Fax:81-3-3812-2910]
COMMENT On Mar 8, 2000 this sequence version replaced gi:6716123.
FEATURES
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CALVASAFAYLHVLNIGLITTTGCTGTWLLSCPPYEHOKRLSILFVSAVLEGA
SVGPLIKVALVDPSILITAFVGTATFAVCSAAMLARREYLYLGLLSSGLSMLM
WLOFASSTFGGASIFKPELYGLLIFVGMVDITQEIIEAHLGDMYVKNLSLFT
DFVAFVRLIILNLSADKEKKKKRN"
BASE COUNT 302 a 213 c 231 g 371 t
ORIGIN
Query Match 41.3%; Score 427.2; DB 8; Length 1117;
Best Local Similarity 73.8%; Pred. No. 4, 4e-103;
Matches 559; Conservative 0; Mismatches 198; Indels 3; Gaps 1;

QY 72 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 131
Db 36 AAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 92

QY 132 AACCGCTGGAGTTAGTTCTCTCAAAAGCTCCGCGAGATCTCACCTCTCGTCAACT 191
Db 93 AGAAGCTGGAGCTATGATTCTCTTAAAGAACTTCCGTCAGATTCTCCAGCCGTTGAGAT 152

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QY 192 CATCTCAAGCAGGTGTACCTTACGCTATGCTGTGCTTTAGTGGCATCGGCTGCTGGGCT 251
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RESULT 6
LOCUS AY114059 775 bp mRNA linear PLN 31-MAY-2002
DEFINITION Arabidopsis thaliana putative Bax inhibitor-1 (At5g47120) mRNA,
complete cds.
ACCESSION AY114059
VERSION AY114059.1 GI:21280946
KEYWORDS FLI CDNA.
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 775)
Yamada, K., Ban, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M.,
Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L.,
Tang, C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L.,
Carinci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,
Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,
Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T.,
Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K.,
Davis, R.W., Ecker, J.R. and Theologis, A.
Arabidopsis Open Reading Frame (ORF) Clones
Unpublished
2 (bases 1 to 775)
Yamada, K., Ban, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M.,
Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L.,

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Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, I., Kamiya, A., Karlin-Neumann, G., Kawai, T., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.

Submitted (16-MAY-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGC (SSP) Consortium members constructed and sequenced the PUNI (ORF) clones using the RAFL cDNAs: Yamada, K., Ban, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.W., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.

Yamada, K. (SSP/PGC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGC) contributed equally to this work as PIs.

FEATURES

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QY 687 GAGAAGGCTCACTTGGTGTATGATTAAGTACGTTAAGCATGCAATGCACTTTTTCACAGAT 746
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RESULT 7

AF390555

LOCUS

Brassica napus Bax inhibitor 1 (BI-1) mRNA linear PLN 16-JUL-2001

DEFINITION

AF390555

ACCESSION

AF390555.1 GI:14719273

VERSION

AF390555.1

KEYWORDS

Brassica napus.

ORGANISM

Brassica napus

REFERENCE

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2 (bases 1 to 1010)

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ORGANISM	Brassica oleracea
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE	1 (bases 1 to 1013)
AUTHORS	Coupe,S.A., Sinclair,B.K., Watson,L.M., Bucknell,T.T. and

REFERENCE
1 (bases 1 to 1013)
Coupe, S.A., Sinclair, B.K., Watson, L.M., Bucknell, T.T. and
AUTHORS

TITLE The isolation and characterization of broccoli homologs to Arabidopsis PCD genes, LSD1 and EI: their role during cell death and senescence

REFERENCE 2 (bases 1 to 1013)

AUTHORS
Coupe, S.R.; Sincclair, D.R.; Hudson, D.M.; Buckmaster, P.H. and
Eason, J.R.

JOURNAL
TIME
DIRECT SUBMISSION
Submitted (29-NOV-2001) Crop and Food Research, Private Bag 11 600,

FEATURES

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117

103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1

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[illegible][illegible]

Case	Age	Sex	Occupation	Duration of symptoms	Site of lesion	Pathological changes	Diagnosis
1	45	Male	Farmer	10 years	Right hand	Chronic inflammation	Chronic pyoderma
2	55	Female	Housewife	5 years	Left hand	Chronic inflammation	Chronic pyoderma
3	65	Male	Retiree	15 years	Right hand	Chronic inflammation	Chronic pyoderma
4	75	Female	Housewife	20 years	Left hand	Chronic inflammation	Chronic pyoderma
5	85	Male	Retiree	25 years	Right hand	Chronic inflammation	Chronic pyoderma
6	95	Female	Housewife	30 years	Left hand	Chronic inflammation	Chronic pyoderma

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Db 418 GGGCAGCAGATGTTGGCGAAGCGCAGAGAGTACCTCTACCTCGGAGACGCTTTCATCTG 477
Qy 553 CGGCTCCCTTCTCTTGTGTGCATCTTCATCTCCATTTTGTGTGTTCCATGGCTG 612
Db 478 GCTTGTCCATGCTTATGTGGCTTCAGTTTGGCTCTTCCATCTTGTGGCTCTGCAATCA 537
Qy 613 TTTTCAAGTTTGTGTTTGTGAGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 672
Db 538 TCTTTRAGTTTGTGCTCTTCTTGTGATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 597
Qy 673 CCCAAGAAATTTTGAAGCTCCTTGTGGTGTATGTGATTTAGTATGATGATGATGATGATG 732
Db 598 CTCAGATATTATAGAGAGCCACCTCGGTGACATGATGATGATGATGATGATGATGATGATG 657
Qy 733 CCTTTTCCAGATTTTGGGCTCTTTTGTGGGATTTCTGATCATCATGTTTAAAGATG 792
Db 658 CCCTTTCCAGATTTTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 717
Qy 793 CATCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 831
Db 718 CGGCAGATAAAGAGATAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 756

RESULT 9
AF453321 1019 bp mRNA linear PLN 27-DEC-2001
LOCUS Brassica oleracea bax inhibitor-like protein (BI2) mRNA, complete
DEFINITION cds.
ACCESSION AF453321
VERSION AF453321.1 GI:17981375
KEYWORDS
SOURCE
ORGANISM Brassica oleracea.
Brassica oleracea.
Brassica oleracea.
REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 1019);
Coupe,S.A., Sinclair,B.K., Watson,L.M., Bucknell,T.T. and
Eason,J.R.,
The isolation and characterization of broccoli homologs to
Arabidopsis PCD genes, LSD1 and BI: their role during cell death
and senescence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1019)
AUTHORS Coupe,S.A., Sinclair,B.K., Watson,L.M., Bucknell,T.T. and
Eason,J.R.
Direct Submission
TITLE Submitted (29-NOV-2001) Crop and Food Research, Private Bag 11 600,
Palmerston North 5301, New Zealand
JOURNAL
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Location/Qualifiers
1..1019
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/db_xref="taxon:3712"
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54..794
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to Arabidopsis thaliana and Homo sapiens bax inhibitor"
/codon_start=1
/product="bax inhibitor-like protein"
/protein_id="AAU50980.1"
/db_xref="GI:17981376"
/translation="MESFSFFFDSPGSRWSVSKLHLQSPVQNLKRVYTLIC
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WGPFLIKVAFDPSIITAFVGTAFIAFCFSGAAMLRREYLYLGLSLGSLMIM
VLQFASIFGGSAGIFKFLYFGLLIIVGVYVVDTEIIEKAHLGMDYVYHALTLFT
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BASE COUNT 246 a 228 c 220 g 325 t
ORIGIN
Query Match 38.6%; Score 399.2; DB 8; Length 1019;

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Best Local Similarity 71.4%; Pred. No. 1.3e-95;
Matches 540; Conservative 0; Mismatches 213; Indels 3; Gaps 1;
Qy 70 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 129
Db 37 AAAGAAAACAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 93
Qy 130 GCACCGCTGGAGATATGATTTCTCAAAAACCTCCGCGCAGATCTCACCTCTCGTTCAAA 189
Db 94 GCAGAGCTGGAGCTATGAATCTCTCAAGAACCTCCATCAGATCTCCCGCTCCGTACAGA 153
Qy 190 CTATCTCAAGCAGGTGTACCTTACGCTATGCTGTCTTTAGTGGCATCGGCTGCTGGGG 249
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Qy 250 CTTACCTTTCACATTTCTATGGAATATCGGTGGCTCTCTCACCAACATTCGATGGGAA 309
Db 214 CTTACCTCCACGGTCTCTGGAACATCGGTGGTATTTCTCACCAACATTCGATGGGAA 273
Qy 310 GCATGTGTGGCTCTCTCAGCTCTCTTATCAAGAGCAAAAAGGCTGCTCTTCTGA 369
Db 274 CCATGATTTGGCTTCTCTCATGTCTCTTATGAGCAACAAAGAGGCTCTCAGCTTCTCT 333
Qy 370 TGGCAGCTGCACCTTTTGAAGCGGCTCTATTGGTCTCTGATTGAGCTGGGCAATTAAT 429
Db 334 TCCTCTCGCGTCTCTTGAAGTGTCTCTGTTGGCCCTTGTATCAAGTGGCTGTGATT 393
Qy 430 TCGATCCAGCATGTGTGTGGGCTTTTGTAGGTGTGCTGTGCTTTTGTGTTGCTCTCT 489
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Db 454 CAGGAGCAGGATTTGGCCAGCAGCAGAGAGATCTCTACCTCGGAGGACTTCTCTCTT 513
Qy 550 CTGGCGTCTCCCTCTCTCTCTGTGTGCATTTTGCATCTCCATTTTGGTGTTCATGG 609
Db 514 CTGCTTGTCCATGCTTATGTGGCTTTCAGTTTGTCTTCTTCCATCTTGTGGCTCTGGT 573
Qy 610 CTGTTTCAAGTTTGAAGTTGTATTTTGGAGTCTTGTGTGTGTGGGCTACATCGTCTTTG 669
Db 574 CCATCTTAAAGTTTGAAGTCTTCTTGGACTCTTGTATCTTTTGGATACATGTTGGTGG 633
Qy 670 ACACCAAGAAATTTTGAAGAGGCTCCTCTGGGTGATGATGATTAAGCATGAT 729
Db 634 ACACCAAGAGATTTATAGAGAAAGCACCTAGGGAGACATGATGTGAACATGATCAT 693
Qy 730 TGACCTTTTTCACAGATTTTGGCGCTGTTTGTGGGATTTCTGATCATGTTTAAAGA 789
Db 694 TGACCTTTTTCACAGATTTTGGCGCTGTTTGTGGGATTTCTGATCATGTTTAAAGA 753
Qy 790 ATGATCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 825
Db 754 ACTCGGAGATAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 789

RESULT 10
AB025926 1181 bp mRNA linear PLN 04-MAR-2000
LOCUS Oryza sativa BI-1 mRNA for Bax inhibitor-1, complete cds.
DEFINITION
ACCESSION AB025926
VERSION AB025926.3 GI:7209771
KEYWORDS Bax inhibitor-1.
SOURCE Oryza sativa (strain:Yamahoushi) cDNA to mRNA.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erihartoideae; Oryzeae; Oryza.
1 (sites)
Kawai,M., Pan,L., Reed,J.C. and Uchimiya,H.
Evolutionally conserved plant homologue of the Bax inhibitor-1
(BI-1) gene capable of suppressing Bax-induced cell death in
yeast(1)

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PERS Lett. 464 (3), 143-147 (1999)
 20086876
 2 (bases 1 to 1181)
 Kawai.M. and Uchimiya.H.
 Direct Submission
 Submitted (06-APR-1999) Hirofumi Uchimiya, University of Tokyo,
 Inst. Mol. Cellu. Biosci., Cellular Function; 1-1-1 Yayoi,
 Bunkyo-ku, Tokyo 113-0032, Japan
 (E-mail: uchimiya@mcmbns.tam.u-tokyo.ac.jp, Tel:81-3-3812-2910,
 Fax:81-3-3812-2910)
 On Mar 8, 2000 this sequence version replaced gi:6759252.
 Sequence updated (02-Mar-2000).
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 ASVPLIKLAVDFDVLGTAIFGTGTAIFAGCTCAAIKAKRELYLGGLLSSGLSL
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 BASE COUNT 262 a 295 c 317 g 307 t
 ORIGIN
 Query Match 33.9%; Score 351; DB 8; Length 1181;
 Best Local Similarity 66.4%; Pred. No. 9.7e-83;
 Matches 504; Conservative 0; Mismatches 255; Indels 0; Gaps 0;
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 DB 106 AGAGAGAGAGAGAGAGAGATGGAGCGCTTCTACTCGACTCGTGGCGTACGGAGCGG 165
 QY 127 CTGCAACCGCTGGAGTTATGATTCTCTCAAAAACCTTCGCCAGATCTCACCTCTCGTTTC 186
 DB 166 CGCGAGCGCTGGGCTACGACTCGCTGAAGAACTTCGCCAGATCTCCCCGCGCTCC 225
 QY 187 AAATCATCTCAAGCAGGTGACCTTAGCTATGCTGTGCTTTAGTGGCATCGGCTGCTG 246
 DB 226 AGTCCACCTCTACGCTCGTTTACCTGCACACTATCGTGGCGCTGGCTGGCGGTGG 285
 QY 247 GGGCTTACCTTCACATTCATCGAATATCGGTGGCGCTCCTCACAAACAATGGCTTGCATGG 306
 DB 286 GCGCATACCTGACGTCGCGCTTGACATCGCGGGATGTTGACTATGCTCGGTGCGTGG 345
 QY 307 GAAGCATGTTGGCTTCTCTCAGCTCCTCTTATCAAGAGCAAAAAGGGTGGCTCTTTC 366
 DB 346 GGAGCATCGCGCTGTTGTTCTCGGTGGCTGTTTGGAGGAGGAGAGGTTTGGGATTC 405
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 DB 406 TCTTGGCGCTGCGCTGCTGGAAAGGGCTTCAGTTGGGCTCTGATCAAGCTTGCCTGAG 465
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Db      128  TTGCACTGGCTCACTGCGGTGGTCTTACTACATTCGCTTGAACATCGCGGGA 187
Qy      283  TCCCTCAACAATGGCTGTGATGGAAGCATGTTGGTGTCTCTCAGTCTCTCTATTC 342
Db      188  TGTGACAAATGCTCGTTGTGCGAACTATCGCTGATGTTCTCGGTGCCAGTCTATG 247
Qy      343  AAGAGCAAAAAGGCTGCTCTCTGATGTCAGTGCACATTTTGAAGCGCTCTATTTG 402
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Qy      703  GTGATATGATAGTTAAGCATGATGACCTTTTCAGATTTGCGGTGTTTGG 762
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Qy      823  GGA 825
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RESULT 12
LOCUS      G73645
DEFINITION RZ957F etiolated leaf tissue of rice Oryza sativa STS genomic clone
VERSION    G73645
KEYWORDS   STS.
SOURCE     Oryza sativa.
ORGANISM   Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 418)
Oryza sativa STS
Oryza sativa (2002)
REFERENCE
AUTHORS    Contact: Susan R. McCouch
JOURNAL    Cornell University
TITLE      Dept. of Plant Breeding, Ithaca, NY 14853-1901, USA
FREETEXT   Tel.: 6072550420

```

```

Fax: 6072556683
Email: srm4@cornell.edu
Primer A: M13 Universal Forward GTAAACGACGCGCCAGT
Primer B: M13 Universal Reverse AACAGCTATGACCATG
STS size: 418
Protocol:
Template: 20-100ng
Primer: 5pmol each
DNTPs: 40nmol
Taq polymerase: 5units
Total volume: 50ul
Buffer:
Tris-HCl: 100mM
KCl: 500mM
MgCl2: 15mM
Gelatin: 0.1%
PH: 8.3

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This is a partial sequence of the RFLP clone named above that was mapped at Cornell University Plant Breeding Dept. and sequenced at the Genome Sequencing Center at Cold Spring Harbor Laboratory. This marker is located on rice chromosome 2. For citations and other related information concerning this probe, please refer to the Gramene database at <http://www.Gramene.org>.

FEATURES

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STs
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BASE COUNT 59 a 118 c 124 g 116 t 1 others
ORIGIN

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Best Local Similarity 65.2%; Pred No. 1-1e-36;
Matches 262; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

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Qy 182 CGTCAAACTCATCTCAAGCAGGTGACCTTACGCTATGCTGTCTTTAGTGGCATCGGC 241
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Qy 362 TCCTTCTGATGCGAGCTGCATTTTGAAGCGCCCTCTATTGCTCTCTGATTGAGCTGG 421
Db 193 GATTCTCTTGGCGCTGCCCTCTGCTGAAGGGGCTTCACTTTGGGCTCTGATCAAGCTTGC 252
Qy 422 CATTAACCTTCGATCCAAAGCATTTGTTGGCGCTTTTGTAGTGTGCTGTGTTTGG 481
Db 253 TGTAGACTTTGACTCAAGCATTTCTCGTAACAGCATTTGTTGGAAGTGCATTTGCA 312
Qy 482 TTGCTTCTCAGCTGCTGCCATGTTGGCAAGGCGCAGGAGTACTTGTACTCTCGGGCT 541
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LOCUS			
DEFINITION Homo sapiens testis enhanced gene transcript protein (TEGT) mRNA,			
complete cds.			
ACCESSION AF033095			
VERSION AF033095.1			
KEYWORDS GI:2645728			
SOURCE			
ORGANISM			
Homo sapiens.			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE			
AUTHORS 1 (Bases 1 to 892)			
TITLE Cowling,R.T. and Birnboim,H.C.			
JOURNAL Direct Submission			
SUBMITTED (05-NOV-1997) Cancer Research Group, Ottawa Regional			
Cancer Centre, 501 Smyth Road, Ottawa, ON K1H 8L6, Canada			
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QY	318	TGCTTCTCTCAGCTCCTCCTTATCAAGAG-----CAAAAAGGGTGCTCTTCTGATG	371
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QY 432 GATCCAAAGCATGTGTTTGGCGCTTTTGTAGGTTGTCTGTGCTGTTTGGTGTCTTCTCA 491
Db 390 AACCCAGCATCTCCCACTGCTTTCATGGCACAGCAATGATCTTTACCTGCTTACC 449
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QY 552 GCGCTCTCCCTCTCTCTGCTGTGCACTTTGGCATCTCCCACTTTTGGTGTCCATGGCT 611
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ACCESSION BC000916
VERSION BC000916.1 GI:13111818
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalob@bcm.tmc.edu.
Villalob, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,
Muzny, D.M., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAP Plate: 3 Row: K Column: 7
This clone was selected for full length sequencing because it
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BASE COUNT 606 a 625 c 602 g 776 t
ORIGIN
Query Match 12.1%; Score 125.2; DB 9; Length 2609;
Best Local Similarity 52.2%; Pred. No. 1.8e-22;
Matches 358; Conservative 0; Mismatches 313; Indels 15; Gaps 3;
QY 144 TATGATTTCTCTAAAAAATTCGCCAGATCTCACCTCTCGTTCAAACTCATCTCAAGCAG 203
Db 93 TTTGATGGCGCTTTTAAATTTTCTCATATAACCCGCTCAAGCAGCAGCACCTGAAGAAG 152
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Tue May 27 10:28:39 2003

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Job time : 2754 secs

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2003, 08:47:18 ; Search time 284 Seconds
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8199.177 Million cell updates/sec

Title: US-09-955-526-3

Perfect score: 1034

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	416.8	40.3	1066	21	Arabidopsis thalia
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4	219.2	21.2	527	22	Testis Enhanced Ge
5	198.4	19.2	712	21	Arabidopsis thalia
6	128.8	12.5	873	22	Bovine mammary tis
7	125.2	12.1	2922	21	Lung cancer associ
8	122	11.8	2600	24	Human CDNA differe
9	122	11.8	2634	19	Bax inhibitor Bi-1

10	83.8	8.1	751	24	ABQ56073	Human ovarian anti
11	77	7.4	380	21	AAC04218	Human secreted pro
12	74	7.2	595	24	ABQ59227	Human colon cancer
13	72	7.0	520	20	AAV86028	EST clone B15. H
14	68.4	6.6	689	24	ABQ60318	Human colon cancer
15	61	5.9	506	24	ABQ58023	Human colon cancer
16	57	5.5	202	19	AAV16142	Microsatellite mar
17	47.8	4.6	6741	21	AAAI0595	Gene encoding a su
18	46.8	4.5	638	23	ABV25317	Human prostate exp
19	43.8	4.2	3654	23	ABLI2508	Drosophila melanog
20	43.8	4.2	3775	23	ABLI2504	Drosophila melanog
21	42.6	4.1	1618	24	ABT04036	Human ovary specif
22	42.4	4.1	752	24	ABQ14854	Oligonucleotide fo
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25	41	4.0	5059	20	AAK84332	Stealth virus nucl
26	40.8	3.9	463	21	AAC03759	Human secreted pro
27	40.8	3.9	2296	19	AAV20662	Barley D-hordein g
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36	38.8	3.8	437	24	ABL63599	Breast cancer rela
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38	38.8	3.8	6487	22	AAI58442	Human polynucleoti
39	38.8	3.8	6491	22	AAH98355	Drosophila EST-der
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ALIGNMENTS

RESULT 1

ABN98455

ID ABN98455 standard; DNA; 1009 BP.

AC ABN98455;

XX

01-AUG-2002 (first entry)

XX Arabidopsis thaliana expressed polynucleotide SEQ ID NO 223.

XX Arabidopsis thaliana; plant; insecticide; fungicide; stress;
XX disease; crop; thale cress; tolerance factor; insect; pathogen;
XX nutrition; ds.

XX Arabidopsis thaliana.

XX US2002023281-A1.

XX 21-FEB-2002.

XX 26-JAN-2001; 2001US-0770445.

XX 27-JAN-2000; 2000US-178472P.

XX (GORL/) GORLACH J.

XX (ANY/) AN Y.

XX (HAMI/) HAMILTON C M.

XX (PRIC/) PRICE J L.

XX (RAIN/) RAINES T M.

XX (YUY/) YU Y.

XX (RAME/) RAMEAKA J G.

XX (PAGE/) PAGE A.

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Qy	672	ACCCAGAAATATTGAGAGGCTCACTTGGGTGATGATGATTACGTTAAGCATGCAATG	731
Db	620	ACACAAGAGATTAGAAAAGCACACCTCGGTGACATGGACTATGTAACAATTCGTTG	679
Qy	732	ACCTTTTCACAGATTTTGGCGCTGTTTTTGTGCGGATCTGATCATCATGTTAAAGAAAT	791
Db	680	ACCTTTTCACTGACTTTTGTAGCTGTGTTTGTTCGGANTCTCATATAATGTTGAAGAAC	739
Qy	792	GCATCTGAGAGGAGAGAGACAGACAGAGAGAGAACT	831
Db	740	TCAGCAGATAAAGAGAGAGAGAGAGAGAGAGAACT	779
RESULT 2			
AAC38715			
ID	AAC38715 standard; DNA, 1066 BP.		
XX	AAC38715;		
NC	AAC38715;		
XX	17-OCT-2000 (first entry)		
DT			
XX	Arabidopsis thaliana DNA fragment SEQ ID NO: 21973.		
DE			
XX	Hybridisation assay; genetic mapping; gene expression control;		
KW	protein identification; signal transduction pathway;		
KW	metabolic pathway; promoter; termination sequence; ss.		
XX	Arabidopsis thaliana.		
OS			
XX	EP1033405-A2.		
FN			
XX	06-SEP-2000.		
PD			
XX	25-FEB-2000; 2000EP-0301439.		
PF			
XX	25-FEB-1999; 99US-0121825.		
FR			
XX	05-MAR-1999; 99US-0123180.		
PR			
XX	09-MAR-1999; 99US-0123548.		
PR			
XX	23-MAR-1999; 99US-0125788.		
PR			

PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
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PR 14-MAY-1999; 99US-0134370.
PR 14-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0138021.
PR 27-MAY-1999; 99US-0138392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
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PR 14-JUN-1999; 99US-0139119.
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PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
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PR 18-JUN-1999; 99US-0139763.
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PR 23-JUN-1999; 99US-0140354.
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PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
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PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 08-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142820.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143342.
PR 14-JUL-1999; 99US-0143624.
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PR 16-JUL-1999; 99US-0144065.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145182.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145218.
PR 26-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
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PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149923.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
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PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.

PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.
PR 29-OCT-1999; 99US-0162143.

Query Match 40.3%; Score 416.8; DB 21; Length 1066;
Best Local Similarity 73.6%; Pred. No. 1.4e-111;
Matches 559; Conservative 0; Mismatches 197; Indels 4; Gaps 2;

QY 72 AAGAGAGAGACATGAGGTTTCATCGTTCCTTCGACGCGCAATCTGCTCTCGC 131
DB 34 AAAAAACGAAACATGATCGGTTCTTCCTTCCTTCGATTCCTCACTG 90
QY 132 AACCGCTGGAGTTATGATTCCTCAAAAACCTCCGCCAGATCTCACCTCTCGTTCAACT 191
DB 91 AGAAGCTGGAGTATGATTCCTCTAAAAACCTCCCTCAGATTCCTCCAGCGCTTCAGAT 150
QY 192 CATCTCAACGAGGTGACCTTACGCTATGCTGCTTTAGTGGCATCGCTGCTGGGCT 251
DB 151 CATCTTAAACGGGTTTATTTGACCTTATGTTGCTCTTGCGGCTGCTGCTTGGAGCT 210
QY 252 TACCTTCACATTCATGGAATATCGTGGCCCTCTTCACAAATGCTTGCANGGGAAGC 311
DB 211 TACCTCCATGTGCTCTGGAATATCGGCGGTATTCCTACACGATTTGATGTTGGAAT 270
QY 312 ATGCTGCTCTCTCTCAGCTCCTCTTATCAAGAGCAAAAAGGCTGCTCTCTCATG 371
DB 271 ATGATTTGGCTCTCTTCATGCTCTCTTATGAACACCAAAAAGGCTTCTCTCTGTT 330
QY 372 GCAGCTGCACATTTTGAAGCGCCTCTATTTGCTCTCTGATGAGCTGGGCAATTAATTC 431
DB 331 GCGTCTGCTGTTCTTCAAGGTGCTCTGTTGGCCCTTGATCAAAAGTGGCAATGATGT 390
QY 432 GATCCAGCATGTTGTTGGCGCTTTTGTAGTGTGCTGCTGTTTGTGCTTCTCA 491
DB 391 GACCCAGCATGCTTATCACTCGTTGTTGGAATGCG-GATACGTTTGTCTGTTCTCA 449
QY 492 GCTGCTGCCATGTTGGCAAGGCGCAGGAGTACTTGTACCTCGGGGCTCTCTTTCATCT 551
DB 450 GCAGCAGCATGTTAGCAAGCAGCAGGAGTATCTACCTTGGAGGACTGCTTTCATCT 509
QY 552 GCGCTCTCCCTCTCTCTGTTGCACTTTCATCTCTCACTTCTTCTGTTGCTTCTGCT 611
DB 510 GCGTGTCTATGTAATGTTGGCTTCCAGTTGCTCTCTGATCTTTGGTGGCTCTGCACT 569
QY 612 GTTTTCAAGTTGAGTTGATTTTGAATCTTCTGTTGTTGTTGTTGTTGTTGTTGTTGAC 671

DB 570 ATCTTTAAGTTTGAGTTGACTTGGACTTTTGATCTTTTGGGATACATGTTGGTGAC 629
QY 672 ACCCAAGAAATTATTGAGAAGGCTCACTTGGGTGATAGATTACGTTAAGCATCCATTG 731
DB 630 ACAAGAGATTATAGAAAAAGCACACCTCGGTGACATGCTATGTAACATTCGTTG 689
QY 732 ACCCTTTTACAGATTTCGCGCTGTTTGTGGGATTCCTCATCATGTTAAAGAAAT 791
DB 690 ACCCTTTTCACTGACTTTAGCTGTTTGTGGATTCATCATATGTTTGAAGAAC 749
QY 792 GCATCTGAGAAGGAAGAAGAAGAAGAAGAAGAGAGAACT 831
DB 750 TCAGCAGATAAAGAGAAGAAGAAGAAGAAGAAGAGAACT 789

RESULT 3
AAF44782
ID AAF44782 standard; cDNA; 884 BP.
XX
AC AAF44782;
XX
XX 27-MAR-2001 (first entry)
DT
XX
XX Testis Enhanced Gene Transcript protein coding sequence #1.
DE
XX
XX Cell death modulator; programmed cell death; PCD; apoptosis;
KW forestry plant; ss.
KW
XX
XX Pinus radiata.
OS
XX
XX WO2000075331-A1.
XX
XX PD 14-DEC-2000.
XX
XX PF 02-JUN-2000; 2000MO-NZ00086.
XX
XX 04-JUN-1999; 99US-0325932.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX
XX Flinn B, Lasham A;
XX
XX WPI; 2001-061724/07.
DR P-PSDB; AAB65755.
XX
XX Novel defender against cell death polynucleotide useful for modulating
PT programmed cell death pathway and specific development pathways in
PT forestry plant -
XX
XX Claim 1; Page 62; 142pp; English.
XX
XX The present invention relates to coding sequences (see AAF44740-F44840
CC and AAF44843-F44844) and proteins (see AAB65714-B65814) involved in
CC programmed cell death (PCD; apoptosis). The coding sequences and proteins
CC of the present invention are useful for modulating a PCD or cell death
CC pathway and various developmental pathways in a forestry plant, by
CC stably incorporating one of the present coding sequences into the genome
CC of the forestry plant, where the coding sequence provides a PCD pathway
CC that is not present in a native form of the forestry plant.
XX
XX Sequence 884 BP; 219 A; 165 C; 216 G; 284 T; 0 other;
SQ

Query Match 21.4%; Score 221.2; DB 22; Length 884;
Best Local Similarity 60.6%; Pred. No. 2.6e-54;
Matches 383; Conservative 0; Mismatches 243; Indels 6; Gaps 1;

QY 203 GGTGTACTTACGCTATGCTGTGTTTGTAGTGGCATCGCTGCTGGGCTTACCTTCACAT 262
DB 4 GGTGTATTTGCTGTAGCTGTGCTTCTGTAACAGCAGCATCGGTGTTTATTGCACT 63
QY 263 TCTATGGAATATGCGTGGCTCTCTCAACAATGCTTGCATGGAGAGCATGCTGTGGCT 322

Db 64 TCTGTTGAATATGAGGCTCTCACGGGCTCGCTTGCATTGCTGTAATCGGGCT 123
QY 323 TCTCTCAGCTCTCTCTT-----ATCAAGAGCAAAAAGGTTGGCTCTTCTGATGGCAGC 376
Db 124 CTTATCCGTCCTTACTCTCTGCAACAATGAGGTAAGAGAGTGGCTGCTCTCGGCGAGC 183
QY 377 TGCACATTTTGAAGGCGCTCTATTGCTCTCTGATTGAGCTGGGCATTAACCTTCGATCC 436
Db 184 TGTGCGTTCAAGGAGCTACTCTGGACCGCTCATCGACGGTCAATTAATATGACTC 243
QY 437 AAGCATGTGTTGGCGCTTTTGTAGTTGTCTGCTGGTTTGTGTTGCTCTCTCAGCTGC 496
Db 244 CAGTATACTGGTGAAGTCTTTGTTGGACCTCTTTGGCCCTTCGCTTCTTTCGGCAGC 303
QY 497 TGCATGTTTGGCAAGCGCAGGAGTACTTGTACTCGGGGCTCTTCTTCATCTGGCT 556
Db 304 AGCAATCACAGCAGAGACGGGAATACCTATTTTGGAGAGATATTGGGCTGGGAAT 363
QY 557 CTCCTCTCTCTCTGCTGCTTGCATCTTGCATCTCTCCATTTTGGTGGTTCATGGCTGTTT 616
Db 364 CAGCATATTGATGGCTGCACTAGCATCTCTCGATTTTGGTGGTCTCTCGGCGAATTA 423
QY 517 CAGATTGAGTGTATTTGGACTCTTGGTGTCTTGGGCTACATCGTCTTTGACACCA 676
Db 424 CACATTGAGATCTCTCGGCTGCTAGTTTCTTGGGTATATATATTATTTGACACA 483
QY 677 AGAATATTGAGAGGCTCACTTGGGTGATATGATTACGTTAAGCATGCAATGACCT 736
Db 484 GATGATCATCGAGAAAGCGACCATGGAGACTATGATTATTTAAACATTCACCTGGACCT 543
QY 737 TTTTCACAGATTTGGCGCTTTTCTGCGGATCTGATCATCATGTTTAAAGATGCATC 796
Db 544 CTTTCATGACTCTGTTGCTGTATTTCTTCCGCTGATGGTCAATATGGCAAGAAATGCAGA 603
QY 797 TGAGAAGGAAGAGAGAAGAAGAAGAGAGAA 828
Db 604 CAGTAAATCCAGGAGGAGGAAAGAGAA 635

RESULT 4

AAF44783

ID AAF44783 standard; cDNA; 527 BP.

XX AAF44783;

XX AAF44783;

XX AAF44783;

DT 27-MAR-2001 (first entry)

XX Testis Enhanced Gene Transcript protein coding sequence #2.

XX Cell death modulator; programmed cell death; PCD; apoptosis;

XX forestry plant; ss.

XX Pinus radiata.

XX Pinus radiata.

XX Pinus radiata.

XX Pinus radiata.

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XX Pinus radiata.

XX Claim 1; Pages 62-63; 142pp; English.
PS The present invention relates to coding sequences (see AAF44740-F44840
XX and AAF44843-F44844) and proteins (see AAF44843-F44844) involved in
CC programmed cell death (PCD; apoptosis). The coding sequences and proteins
CC of the present invention are useful for modulating a PCD or cell death
CC pathway and various developmental pathways in a forestry plant, by
CC stably incorporating one of the present coding sequences into the genome
CC of the forestry plant, where the coding sequence provides a PCD pathway
CC that is not present in a native form of the forestry plant.
XX

SQ Sequence 527 BP; 98 A; 148 C; 143 G; 138 T; 0 other;

Query Match 21.2%; Score 219.2; DB 22; Length 527;

Best Local Similarity 74.5%; Pred. No. 7.7e-54;

Matches 289; Conservative 0; Mismatches 98; Indels 1; Gaps 1;

QY 130 GCAACGGTGGAGTTATGATCTCTCAAAACTTCCGCCAGATCTCACCTCTCGTTCAAA 189

Db 141 GCAAGGGTGGAGCCACGATTCCTCAAGAACTTCCGCCAGATATCTCCGCCGCTCCAAT 200

QY 190 CTCATCTCAAGCAGGTGTACTTACGCTATGCTGCTTGTAGTGGCATCGGCTCGGG 249

Db 201 CTCATCTCAAGCAGGTGTACTTACGCTATGCTGCTTGTAGTGGCATCGGCTCGGG 260

QY 250 CTTACTCTCACATTTCTATGGAATATCGGTGGCTCTTCAACAATCGCTTGCATGGAA 309

Db 261 CTTACTCTCACATTTCTATGGAATATCGGTGGCTCTTCAACAATCGCTTGCATGGAA 320

QY 310 GCATGCTGGCTCTCTCTCAGCTCTCTCTTATCAGAGCAAAAAGGTTGGCTCTTCTGA 369

Db 321 GCATGCTGGCTCTCTCTCAGCTCTCTCTTATCAGAGCAAAAAGGTTGGCTCTTCTGA 380

QY 370 TGGCAGCTGCACATTTTGAAGCGGCTCTTATGGTCTCTGATTTGAGCTGGGCAATTAAC 429

Db 381 TGGCAGCTGCACATTTTGAAGCGGCTCTTATGGTCTCTGATTTGAGCTGGGCAATTAAC 440

QY 430 TCGATCCAGCATTTGTTGGCGCTTTTGTAGTTGCTGCTGCTGCTGCTGCTGCTGCT 489

Db 441 TCGATCCAGCATTTGTTGGCGCTTTTGTAGTTGCTGCTGCTGCTGCTGCTGCTGCT 500

QY 490 CAGCTGCTGCCATTTTGAAGCGGCTCTTATGGTCTCTGATTTGAGCTGGGCAATTAAC 517

Db 501 CAGCTGCTGCCATTTTGAAGCGGCTCTTATGGTCTCTGATTTGAGCTGGGCAATTAAC 527

RESULT 5

AAC51940

ID AAC51940 standard; DNA; 712 BP.

XX AAC51940;

XX AAC51940;

XX AAC51940;

XX AAC51940;

XX AAC51940;

XX AAC51940;

XX AAC51940;

XX AAC51940;

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XX AAC51940;

XX AAC51940;

XX AAC51940;

Arabidopsis thaliana DNA fragment SEQ ID NO: 70058.

Hybridisation assay; genetic mapping; gene expression control;

protein identification; signal transduction pathway;

metabolic pathway; promoter; termination sequence; ss.

Arabidopsis thaliana.

EP1033405-A2.

06-SEP-2000.

25-FEB-2000; 2000EP-0301439.

25-FEB-1999; 99US-0121825.

05-MAR-1999; 99US-0123180.

09-MAR-1999; 99US-0123548.

23-MAR-1999; 99US-0125788.

PR	25-MAR-1999;	99US-0126264.	PR	16-JUL-1999;	99US-0144086.
PR	29-MAR-1999;	99US-0126785.	PR	19-JUL-1999;	99US-0144325.
PR	01-APR-1999;	99US-0127462.	PR	19-JUL-1999;	99US-0144331.
PR	08-APR-1999;	99US-0128234.	PR	19-JUL-1999;	99US-0144332.
PR	16-APR-1999;	99US-0128714.	PR	19-JUL-1999;	99US-0144333.
PR	19-APR-1999;	99US-0129845.	PR	19-JUL-1999;	99US-0144334.
PR	21-APR-1999;	99US-0130077.	PR	19-JUL-1999;	99US-0144335.
PR	23-APR-1999;	99US-0130449.	PR	20-JUL-1999;	99US-0144352.
PR	23-APR-1999;	99US-0130510.	PR	20-JUL-1999;	99US-0144352.
PR	28-APR-1999;	99US-0130891.	PR	20-JUL-1999;	99US-0144632.
PR	30-APR-1999;	99US-0131449.	PR	20-JUL-1999;	99US-0144632.
PR	30-APR-1999;	99US-0132048.	PR	21-JUL-1999;	99US-0144884.
PR	04-MAY-1999;	99US-0132407.	PR	21-JUL-1999;	99US-0144814.
PR	05-MAY-1999;	99US-0132484.	PR	21-JUL-1999;	99US-0145086.
PR	06-MAY-1999;	99US-0132486.	PR	22-JUL-1999;	99US-0145088.
PR	06-MAY-1999;	99US-0132486.	PR	22-JUL-1999;	99US-0145085.
PR	07-MAY-1999;	99US-0132487.	PR	22-JUL-1999;	99US-0145087.
PR	11-MAY-1999;	99US-0132863.	PR	22-JUL-1999;	99US-0145089.
PR	14-MAY-1999;	99US-0134256.	PR	22-JUL-1999;	99US-0145192.
PR	14-MAY-1999;	99US-0134218.	PR	23-JUL-1999;	99US-0145145.
PR	14-MAY-1999;	99US-0134219.	PR	23-JUL-1999;	99US-0145218.
PR	14-MAY-1999;	99US-0134221.	PR	26-JUL-1999;	99US-0145224.
PR	14-MAY-1999;	99US-0134370.	PR	27-JUL-1999;	99US-0145276.
PR	19-MAY-1999;	99US-0134768.	PR	27-JUL-1999;	99US-0145913.
PR	20-MAY-1999;	99US-0134941.	PR	27-JUL-1999;	99US-0145918.
PR	21-MAY-1999;	99US-0135124.	PR	27-JUL-1999;	99US-0145919.
PR	21-MAY-1999;	99US-0135353.	PR	28-JUL-1999;	99US-0145951.
PR	24-MAY-1999;	99US-0135629.	PR	02-AUG-1999;	99US-0146386.
PR	25-MAY-1999;	99US-0136021.	PR	02-AUG-1999;	99US-0146388.
PR	27-MAY-1999;	99US-0136392.	PR	02-AUG-1999;	99US-0146389.
PR	28-MAY-1999;	99US-0136782.	PR	03-AUG-1999;	99US-0147038.
PR	01-JUN-1999;	99US-0137222.	PR	04-AUG-1999;	99US-0147204.
PR	03-JUN-1999;	99US-0137528.	PR	05-AUG-1999;	99US-0147302.
PR	04-JUN-1999;	99US-0137502.	PR	05-AUG-1999;	99US-0147192.
PR	07-JUN-1999;	99US-0137724.	PR	06-AUG-1999;	99US-0147260.
PR	08-JUN-1999;	99US-0138094.	PR	06-AUG-1999;	99US-0147303.
PR	10-JUN-1999;	99US-0138540.	PR	08-AUG-1999;	99US-0147416.
PR	10-JUN-1999;	99US-0138847.	PR	09-AUG-1999;	99US-0147493.
PR	14-JUN-1999;	99US-0139119.	PR	09-AUG-1999;	99US-0147935.
PR	16-JUN-1999;	99US-0139452.	PR	10-AUG-1999;	99US-0148171.
PR	16-JUN-1999;	99US-0139453.	PR	11-AUG-1999;	99US-0148319.
PR	17-JUN-1999;	99US-0139492.	PR	12-AUG-1999;	99US-0148341.
PR	18-JUN-1999;	99US-0139454.	PR	13-AUG-1999;	99US-0148565.
PR	18-JUN-1999;	99US-0139455.	PR	13-AUG-1999;	99US-0148684.
PR	18-JUN-1999;	99US-0139456.	PR	16-AUG-1999;	99US-0145368.
PR	18-JUN-1999;	99US-0139457.	PR	17-AUG-1999;	99US-0149175.
PR	18-JUN-1999;	99US-0139458.	PR	18-AUG-1999;	99US-0149426.
PR	18-JUN-1999;	99US-0139459.	PR	20-AUG-1999;	99US-0149722.
PR	18-JUN-1999;	99US-0139460.	PR	20-AUG-1999;	99US-0149723.
PR	18-JUN-1999;	99US-0139461.	PR	20-AUG-1999;	99US-0149723.
PR	18-JUN-1999;	99US-0139462.	PR	23-AUG-1999;	99US-0149929.
PR	18-JUN-1999;	99US-0139463.	PR	23-AUG-1999;	99US-0149902.
PR	18-JUN-1999;	99US-0139750.	PR	25-AUG-1999;	99US-0149930.
PR	18-JUN-1999;	99US-0139763.	PR	26-AUG-1999;	99US-0150566.
PR	21-JUN-1999;	99US-0139817.	PR	26-AUG-1999;	99US-0150884.
PR	22-JUN-1999;	99US-0139899.	PR	27-AUG-1999;	99US-0151066.
PR	23-JUN-1999;	99US-0140353.	PR	27-AUG-1999;	99US-0151066.
PR	23-JUN-1999;	99US-0140354.	PR	30-AUG-1999;	99US-0151080.
PR	24-JUN-1999;	99US-0140695.	PR	31-AUG-1999;	99US-0151303.
PR	28-JUN-1999;	99US-0140823.	PR	01-SEP-1999;	99US-0151438.
PR	29-JUN-1999;	99US-0140931.	PR	07-SEP-1999;	99US-0151930.
PR	30-JUN-1999;	99US-0141287.	PR	10-SEP-1999;	99US-0152363.
PR	01-JUL-1999;	99US-0141842.	PR	13-SEP-1999;	99US-0153070.
PR	01-JUL-1999;	99US-0141842.	PR	15-SEP-1999;	99US-0153758.
PR	02-JUL-1999;	99US-0142154.	PR	16-SEP-1999;	99US-0154018.
PR	06-JUL-1999;	99US-0142055.	PR	16-SEP-1999;	99US-0154039.
PR	08-JUL-1999;	99US-0142390.	PR	22-SEP-1999;	99US-0154779.
PR	09-JUL-1999;	99US-0142803.	PR	23-SEP-1999;	99US-0155139.
PR	12-JUL-1999;	99US-0142920.	PR	23-SEP-1999;	99US-0155486.
PR	13-JUL-1999;	99US-0143677.	PR	24-SEP-1999;	99US-0155659.
PR	14-JUL-1999;	99US-0143624.	PR	28-SEP-1999;	99US-0156458.
PR	15-JUL-1999;	99US-0144005.	PR	28-SEP-1999;	99US-0156596.
PR	16-JUL-1999;	99US-0144085.	PR	04-OCT-1999;	99US-0157117.
			PR	05-OCT-1999;	99US-0157753.
			PR	06-OCT-1999;	99US-0157865.
			PR	07-OCT-1999;	99US-0158029.

[illegible]

RESULT 6
AAAF92293
ID: AAAF92293 standard; cDNA: 873 BP.

AC AAF92293;

XX	15-MAY-2001	(first entry)
DT		

XX
DE Bovine mammary tissue derived cDNA #6.

XX	Bovine; mammary gland; cancer; tumour; angiogenesis; ss.
KW	
XX	
OS	Bos taurus.
XX	
PN	WO200114553-A1.
XX	
XX	
PD	01-MAR-2001.
XX	
PF	23-AUG-2000; 2000WO-NZ00166.
XX	
PR	23-AUG-1999; 99US-0150330.
XX	
PA	(GENE-) GENESIS RES & DEV CORP LTD.
XX	(NZPA-) NEW ZEALAND PASTORAL AGRIC RES INST LTD.
PA	
PI	Havukkala IU, Gleen M, Grigor MR, Molenaar AJ;
XX	
DR	WPI; 2001-226619/23.
XX	
PT	New polypeptides and polynucleotides encoding the polypeptides, which
PT	are expressed in bovine mammary gland tissue, useful for stimulating
PT	mammary gland growth or function, or inducing differentiation of milk
PT	producing cells -
XX	
PS	Claim 1; Page 43; 97pp; English.
XX	
CC	The present invention relates to proteins derived from bovine
CC	mammary gland cells. The invention is useful for stimulating
CC	bovine mammary gland cell growth and function, inhibiting the
CC	growth of various mammary gland cancer cells, inhibiting
CC	angiogenesis and vascularization of tumours, or modulating
CC	the growth of blood vessels in a mammal.
XX	
SQ	Sequence 873 BP; 206 A; 218 C; 196 G; 253 T; 0 other;

Query Match 12.5%; Score 128.8; DB 22; Length 873;
Best Local Similarity 52.5%; Pred. No. 3.1e-27;
Matches 386; Conservative 0; Mismatches 328; Indels 21; Gaps

144	QY	TATGATTCCTCAAAAATCTTCGCGAGATCTCACTCTGCTTAACTCATCTCAAGAG	203
58	Db	TTTGATGCACTCTTTAAATTTTCCACATAACCCCTCGACACAGCAGCACCTGAAGAAG	117
204	QY	GTGTACCTTACGCTATGCTGTGCTTTAGTGGCATCGGCTGCTGGGGCTTACCTTCA	259
118	Db	GTATTATGCCAGTTTGCCCTCTGATGTTTGTGGCGGCTCGGGGGCCTATATCCATG	177
260	QY	--CAATTATGGAAATACGGTGGCTCTCAACAATGGCTTGCTATGGGAGCATGGTG	317
178	Db	GTACACCATTTCAATCAGGCTGGCCTGCTCTGCTCTTGGGCTCTTTGGGGTTGATGATT	237
318	QY	TGGCTTCTCTCAGCTCCTCTCTATTCAAG-----AGCAAAAAAGGGTGGCTCTCTGATG	371
238	Db	TGGCTGATGGCACACCTCACAGCCATGAACTGAGCAGCAAAAGACTGGGACTTCTGGCT	297
372	QY	GCAGCTGCACCTTTTGAAGCGCTCTATTGGTCTCTGATTTGAGCTGGGCATTAACTTC	431
298	Db	GGATTTGGCTTTCCCTTACAGAGTTGGCCTGGGCCCTGCTCTGGACTTGTGCATTGGCATT	357
432	QY	GATCCAGACATGTTTGGCGCTTTTGTAGTGTGCTGTGGTTTTGGTTGCTCTCTCA	491
358	Db	AACCCAGCATCTTCCCACTGCCTTCATGGGCACAGCAATGATCTTCACCTGCTTCAC	417
492	QY	GCTGCTGCCATGTTGGCAAGGCGCAGGGAGTACTGTACCTCGGGGCCCTCTTTCACT	551
418	Db	CTGAGTGCACCTCTATGCCAGGCGCCGTAGCTACCTCTTTCTAGGAGGTATCTTGATGTGG	477
552	QY	GGGCTCTCCCTCTCTCTCTGGTGACATTGCATCCCTCCATTTTTGGTGGTCCATGGCT	611
478	Db	GCCATGAGCCCTCACTGCTCTTGCTTCCCTTGG---GGAAACCTTTTCTTCGGATCTGTTGG	534
612	QY	GTTTTCAAGTTTGAGTTGTAATTTTGGACTCTTGGTGTGTTGGGGCTACATCGCTTTTGAC	671

KW fungal infection; sterile inflammatory disease; psoriasis;
 KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
 KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
 KW adult respiratory distress syndrome; inflammatory bowel disease;
 KW Crohn's disease; ulcerative colitis; periodontal disease;
 KW granulocyte activation; chronic inflammation; allergy.

OS Homo sapiens.

XX WO200228999-A2.

XX 11-APR-2002.

XX 03-OCT-2001; 2001WO-US030821.

XX 03-OCT-2000; 2000US-237189P.

XX (GENE-) GENE LOGIC INC.

XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
 DR WPI; 2002-435328/46.

XX Detecting granulocyte activation by detecting differential expression
 PT of genes associated with granulocyte activation, which serves as
 PT diagnostic markers that is useful for monitoring disease states and
 PT drug toxicity -

XX Claim 1; SEQ ID No 1229; 114pp; English.

XX The invention relates to detecting (M1) granulocyte (GC) activation
 CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
 CC DNA chip analysis as given in the specification, and comparing
 CC the expression level to an expression level in an unactivated
 CC GC, where differential expression of Gs is indicative of GCA.
 CC Also included are modulating (M2) Gs by contacting GC with an agent
 CC that alters the expression of at least one gene in Gs; (2) screening (M3)
 CC for an agent capable of modulating GCA or an inflammation (especially
 CC chronic) in a tissue, an allergic response in a subject, exposure of a
 CC subject to a pathogen or sterile inflammatory disease using the
 CC gene expression profile; (3) detecting (M4) an inflammation (especially
 CC chronic) in a tissue, an allergic response in a subject, exposure of a
 CC subject to a pathogen or sterile inflammatory disease, by detecting a
 CC level of expression in a sample of the tissue of gene(s) from Gs, where
 CC the level of expression of the gene is indicative of inflammation;
 CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
 CC an allergic response in a subject, exposure of a subject to a pathogen
 CC or sterile inflammatory disease, by contacting a tissue having
 CC inflammation with an agent that modulates the expression of gene(s)
 CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
 CC modulating Gs; M3 is useful for screening an agent capable of modulating
 CC GCA preferably in an inflammation in a tissue; M4 is useful for
 CC detecting an inflammation (especially chronic) in a tissue, an allergic
 CC response in a subject, exposure of a subject to a pathogen or sterile
 CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
 CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
 CC reperfusion injury, ARDS, adult respiratory distress syndrome,
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
 CC periodontal disease; also bacterial infection, viral infection,
 CC parasitic infection, protozoal infection, fungal infection and M5 is
 CC useful for treating one of the above conditions. The present
 CC sequence represents a gene differentially expressed in granulocytes.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 2600 BP; 619 A; 621 C; 590 G; 770 T; 0 other;

XX Query Match 11.8%; Score 122; DB 24; Length 2600;

XX Best Local Similarity 51.9%; Pred. No. 5.3e-25;

XX Matches 356; Conservative 0; Mismatches 315; Indels 15; Gaps 3;

QY 144 TATGATCTCTCAAAAACCTCCGCGAGATCTCACTCTCGTTCAAACTCATCTCAAGCAG 203
 Db 68 TTGTATGCGCTTTTAAATTTTCTCATATAACCCGTCACAGCAGCAGCAGCAGTGAAG 127
 QY 204 GTCTACCTTACGCTATGCTGCTTTAGTGGCATCGGCTGCTGGGGCTTACTTCA---- 259
 Db 128 GTCTATGCGAAGTTTTCCTTTGTAAGTTTGGGGGCTGAGGGGCTATGTCATATG 187
 QY 260 --CATTTCTATGAATATCGGTGGCTCTCTCAACAATATGGCTTGCATGGGAAGCATGGT 317
 Db 188 GTCACTCAATTCATTGAGGCTGGCTGCTGCTGCTGGGCTCCCTGATATTTGATGAT 247
 QY 318 TGGCTTCTCTCAGCTCCTCTTATCAAGAG-----CAAAAAAGGCTGCTCTCTCTGATG 371
 Db 248 TGGCTGATGGCAACCTCTATAGCCATGAACCTGAACAGAAAGACTGGGACTTCTTGCT 307
 QY 372 GCAGCTGCACATTTTGAAGCGCCTCTATTTGGTCTCTGATTTGAGCTGGGCGCTTCTTTCA 431
 Db 308 GGATTTGCATTTCTTACAGGAGTTGGCCTGGGCGCTGCGCTGGAGTTTTTGTATTGCTG 367
 QY 432 GATCCAAAGCATTTGTTGGCGCTTTTGTAGTTGCTGTTGTTGGTTGGTTGCTTCTCA 491
 Db 368 AACCCAGCATCTCTCCCACTGCTTTTCATGGGCAAGCAATGATCTTTTACCTGCTTACC 427
 QY 492 GCTGCTGCCATGTTGGCAAGGCGCAGGAGTACTTTGTACCTCGGGGGCTTCTTTTCACT 551
 Db 428 CTCAGTGCACCTCTATGCCAGGCGCTAGCTACTCTTTCCTGGGAGGTATCTTGATGCA 487
 QY 552 GGGCTCTCCCTCTCTCTGTTGGTGCATTTGATCTCTCACTTTTGGTGGTTCATGGCT 611
 Db 488 GCGCTGAGTTGTTGTTTTGTTCTTCCCTGGGGAAT---GTTTTCTTTGGATCCATTGG 544
 QY 612 GTTTTCAAGTTTGAGTTGATTTTGGACTCTTTGGTGTGTTGGGCTACATCGTCTTTTGAC 671
 Db 545 CTTTCCAGGCAACCTGATGTTGGGACTTGGTGGTCTGTTGGCTTCGTTCTTCTTGAT 604
 QY 672 ACCCAAGAAATATTGAGAAGGCTCATTGGGTGATGATGATTAGCTTAAGCATGCATTG 731
 Db 605 ACTCAACTCATTTATTTAAAAAGGCCGAACATGGAGATCAAGATTATATCTGGCAGCTGC 664
 QY 732 ACCCTTTTACAGATTTTGGCGCTGTTTTTGTGGGATTCTGATCATCATGTTAAAGAAAT 791
 Db 665 GATCTCTTCTAGATTTTCACTTCTTTCAGAAACTCATGATGATCTCTGGCCATGAT 724
 QY 792 GCATCTGAGAAGGAAGAAAGAAAGAA 817
 Db 725 GAAAAGGATAAGAAAGAAAGAAAGAA 750

RESULT 9

AAV59067

ID AAV59067 standard; cDNA; 2634 BP.

XX AC AAV59067;

XX 02-FEB-1999 (first entry)

XX Bax inhibitor BI-1 cDNA.

XX Bax inhibitor; BI-1; human; apoptosis; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 73..786

XX /tag= a

XX WO9840397-A1.

XX 17-SEP-1998.

XX 13-MAR-1998; 98NC-US05015.

XX

PR 14-MAR-1997; 97US-0818514.
XX (BURN-) BURNHAM INST.
PA Reed JC, Xu Q;
XX WPI; 1998-531519/45.
DR P-PSDB; AAW73136.
XX
XX Bax inhibitor proteins, BI-1 and BI-2 - useful e.g. to modulate
PT cellular apoptotic activity or identify agents altering BI-1 or BI-2
PT binding which can modulate apoptotic activity
XX
XX Claim 2; Page 61-63; 80pp; English.
XX
XX This cDNA clone codes for an inhibitor protein, termed BI-1 (see
CC AAW73136), of the pro-apoptotic protein Bax. Nucleic acids encoding
CC BI-1 and BI-2 (see AAW59068) were identified by suppression of
CC Bax-induced death of yeast cells transformed to express human Bax.
CC A human HepG2 cDNA library was used for library screening. The
CC invention provides vectors, optionally expression or viral vectors,
CC containing BI nucleic acids, and host cells containing these
CC vectors. The nucleic acids encoding BI-1/BI-2 can be used to
CC increase expression of these proteins in cells, or antisense
CC molecules prepared from them used to decrease expression. In
CC these ways, cellular apoptotic activity may be modulated (claimed).
CC The nucleic acids and complementary sequences are also useful as
CC probes to detect BI-encoding nucleic acid molecules in samples.
XX
XX Sequence 2634 BP; 632 A; 626 C; 597 G; 779 T; 0 other;
SQ

Query Match 11.8%; Score 122; DB 19; Length 2634;
Best Local Similarity 51.9%; Pred. No. 5.4e-25;
Matches 356; Conservative 0; Mismatches 315; Indels 15; Gaps 3;

QY 144 TATGATTTCTCAAAATCTCCGACATCTCAGCTCTGCTTCAAACTCATCTCAAGCAG 203
DB 100 TTGATGCGCTTTTAAATTTTCTCATATAACCCCGTCAACGACGACGACCTGAAGAAG 159
QY 204 GTGATCTTACGCTATGCTGTCTTTAGTGCATCGCTGCTGGGCTTACCTTCA ---- 259
DB 160 GTCATGCAAGTTTTCCTTTGATGTTTGTGGCGCTGCAGGGGCTATGTCATATG 219
QY 260 --CATCTATGATATCGTGGCTCTCTCAACAATGCTTGCATGGGAACATGGTG 317
DB 220 GTCACATATTCATTCAGGCTGGGCTGCTGTCTGCTGGGCTCCCTGATTTGATGATT 279
QY 318 TGGCTTCTCTAGCTCTCTCTTATCAAGAG-----CAAAAAGGGTGGCTCTTCTGATG 371
DB 280 TGGCTGATGCAACACCTCATAGCATGAACCTGAACAGAAACCTGGACCTTCTGCT 339
QY 372 GCAGCTGCACTTTTGAAGGCGCTCTATTGCTCTGATTGAGCTGGGCATTAACCTC 431
DB 340 GGATTTGCATTCCTTACAGGAATTGGGCTGGGCGCTGCCCTGGAGTTTGTATGCTGTC 399
QY 432 GATCAAGCATTTGTTGGGCGCTTTTGTAGTGTGTGCTGTTGTTTGTGCTTCTCA 491
DB 400 AACCCAGCATCTTCCACATGCTTTTCAATGGCAGCGGCAATGATCTTTACTGCTTCA 459
QY 492 GCTGCTGCATTTTGGCAAGGCGGAGGAGTACTGTACCTCGGGGCGCTTCTTCACT 551
DB 460 CTCAGTGCACTTATGCCAGGCGGCTAGTACCTCTTCTGGGAGGTATCTTGAATGCA 519
QY 552 GGGCTCTCCTCTCTCTGTTGTGACATTTGATCTCCATTTTGTGTTTCCATGGCT 611
DB 520 GCGCTGAGTTGTTGCTTTTGTCTTCCCTGGGAT---GTTTCTTGGATCATTTGG 576
QY 612 GTTTTCAAGTTGAGTTGATTTGAGCTCTTGGTGTGTTGGCTACATGCTTTGAC 671
DB 577 CTTTTCAGGCAAACTGTATGAGGCTGGTGGTGTGCTGCTGCTTTTGTAT 636
QY 672 ACCAAGAAATATTGAGAGGCTCACTTGGGTGATATGGATTACCTTAAGCATGATTG 731

DB 637 ACTCAACTCATTTTGAAGGCGGACATGAGATCAAGATTATATCTGGCACTGCATT 696
QY 732 ACCCTTTTACAGATTTTGGCGCTCTTTTGTGGGATTCGTGATCATCATCTTAAAGAT 791
DB 697 GATCTCTTCTTGAATTTCTTCTTCTTCAAAAACCTCATGATGATCTGCGCATGAAT 756
QY 792 GCATCTGAGAGGAGAGAGAGAGAA 817
DB 757 GAAAGGATAAGAGAGAGAGAGAA 782

RESULT 10
ABQ56073
ID ABQ56073 standard; cDNA; 751 BP.
XX
XX AC ABQ56073;
DT 22-AUG-2002 (first entry)
XX
XX DE Human ovarian antigen HPDWT56 cDNA, SEQ ID NO:1953.
XX
XX KW Human: ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200200677-A1.
XX
XX PD 03-JAN-2002.
XX
XX EF 07-JUN-2001; 2001WO-US18569.
XX
XX PR 07-JUN-2000; 2000US-209467P.
XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Birse CE, Rosen CA;
XX
XX DR WPI; 2002-147878/19.
XX
XX DR P-PSDB; ABP42996.
XX
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
XX useful in the prevention, treatment and diagnosis of cancer (e.g.
XX ovarian cancer), immune disorders, cardiovascular disorders and
XX neurological diseases.
XX
XX PS Claim 1; SEQ ID NO 1953; 2922pp; English.
XX
XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
XX ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
XX encompasses polypeptides 90% identical and polynucleotides 95% identical
XX to the sequences of the invention. The invention additionally relates to
XX recombinant vectors and host cells comprising human ovarian antigen
XX polynucleotides, antibodies against human ovarian antigens, and the use
XX of ovarian antigen polynucleotides and polypeptides in diagnosing,
XX treating, prognosing or preventing various ovary and/or breast-related
XX disorders. Such conditions include ovarian cancer and breast cancer, and
XX metastatic tumours of ovarian or breast origin, reproductive system
XX disorders (e.g., infertility, disorders of pregnancy, anovulation,
XX polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
XX disorders, infections (e.g., chlamydia, HIV, toxoplasmosis), and toxic
XX shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
XX vaginitis), immune disorders (e.g., congenital and acquired
XX immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
XX blood-related disorders (e.g., anaemia), cardiovascular disorders,

IC respiratory disorders, neurological disorders, gastrointestinal disorders
IC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents cDNA encoding a human ovarian antigen of the
CC invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 751 BP; 163 A; 177 C; 185 G; 225 T; 1 other;

Query Match 8.1%; Score 83.8; DB 24; Length 751;
Best Local Similarity 50.6%; Pred. No. 4.3e-14;
Matches 312; Conservative 0; Mismatches 288; Indels 16; Gaps 4;
QY 144 TATGATCTCTCAAAACCTTCGCGAGATCTCACCTCTCGTTCAAACTCATCTCAAGCAG 203
DB 93 TTGATGCGCTTTAAATTTCTCATATAACCCGTCACGACGACACCTGAAGAAG 152
QY 204 GTGACCTTACGCTATGCTGTCTTTAGTGGATCGGCTGCTGGGGCTTACCTTCA 259
DB 153 GTCTATGCAAGTTTTCGCCCTTTGTATGTTTGGCGGCTGCAGGGCCCTATGTCCATATG 212
QY 260 --CATCTTATGGAATATCGTGGCTCCCTCAACAATGGCTTGCATGGGAAGCATGGTG 317
DB 213 GTCACTCATTTCAATTCAGCTGGCTGCTGTCTGGCTCCCTCATATTGATGATT 272
QY 318 TGCGTCTCTAGCTCTCTCTATCAAGAG-----CAAAAGGGTGGCTCTCTGATG 371
DB 273 TGGCTGATGGCAACACTCATAGCCATGAACATGAACAGAAAGACTGGGACTCTTGTCT 332
QY 372 GCAGCTGCATTTTGAAGCGGCTCTATTGCTCTGATTTGAGCTGGGCAATTAACCTTC 431
DB 333 GATTTGCAATCTTACAGAGTGTGCTGGCCCTGGCCCTGGAGTTTGTATGCTGTC 392
QY 432 GATCCAGCATTTGTTGGCGCTTTTGTAGGTGTGCTGGTTTGGTTGCTCTCTCA 491
DB 393 AACCCAGCATCTCTCCCACTGTCTTTCATGGGCGACGGCAATGATCTTTACCTGTCTCAC 452
QY 492 GCTGCTGCCATGTTGCAGGCGCAGGAGTACTGTACTCTCGGGGCTCTTTTCATCT 551
DB 453 CTGAGTGCACTATGCGAGGCGCCCTAGCTACCTCTTCTGGGAGGATCTGTATGATCA 512
QY 552 GGGGTCTCCCTCTCTCTGTTGACATTTGCACTCTCCATTTTGGTGGTTCATGGCT 611
DB 513 AGCCCTGAGCTTGGTGTCTTGTCTCCCTGG---GGAATGTTTCTTTGGATCCATTGG 569
QY 612 GTTTTCAAGTTTGAGTTGATTTTGGACTCTTGGTGTGTTGGCTACATCGTCTTTGAC 671
DB 570 CTTTTCAGGCAACCTGTATNTGGGACTGGTGGTCAATGTGGGCTC-GCCTTTTGTAT 628
QY 672 ACCCAAGAAATTTAGAGAGGCTCACTTGGGTGATATGGATATCGTTAAGCATCATTTG 731
DB 629 ACTCAACTATTATGAAGAGCCGACATGGAGATCAAGATTATATCTGGCACTGCAATT 688
QY 732 ACCCTTTTCAGATT 747
DB 689 GATCTCTCTTAAGATT 704

RESULT 11
AAC04218
ID AAC04218 standard; cDNA; 380 BP.
XX
AC AAC04218;
XX AC
XX AC
DT 06-OCT-2000 (first entry)
XX

DE Human secreted protein 5' EST, SEQ ID NO: 8293.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW Gene therapy; chromosome mapping; ss.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-0200610.
XX
PR 26-FEB-1999; 99US-0122487.
XX
PA (GEST) GENSET.
XX
PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX
DR WPI; 2000-500381/45.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
PS Claim 1; SEQ ID 8293; 71pp + CD-ROM; English.
XX
CC The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors.
XX
SQ Sequence 380 BP; 88 A; 88 C; 81 G; 121 T; 2 other;

Query Match 7.4%; Score 77; DB 21; Length 380;
Best Local Similarity 53.7%; Pred. No. 3e-12;
Matches 180; Conservative 1; Mismatches 151; Indels 3; Gaps 1;
QY 483 TGGTTCTAGCTGCTGCCATGTTGCAAGCGCGAGGAGTACTGTACTCGGGGCTT 542
DB 2 TGGTTCACTCAGTGCATCTATGCCAGGCGCGGTAGCTACCTCTTCTGGGAGGATC 61
QY 543 CTTTTCATCGGGTCTCCCTTCTCTCTGTTGCACTTTGCATCTCCTCATTTTGGTGGT 602
DB 62 TTGATGTACCCCTGAGCTTGTGCTTTTGTCTTCCCTGG---GGAATGTTTCTTTGGA 118
QY 603 TCCATGGCTGTTTCAAGTTTGAAGTTGATTTTGGACTCTCTGGTGTGTTGGGCTACATC 662
DB 119 TCCATTTGGCTTTTCCAGGCAACCTGTATGTGGGACTGGTGGTCAATGTGGTCTTGGT 178
QY 663 GTCCTTGACACCCCAAGAAATATTGAGAGGCTCACTGGGTGATATGATTAAGTTAAG 722
DB 179 CTTTGTGATCTCACTCATTTATGAAAGCCGACATGGGATCAAGATTATATCTGG 238
QY 723 CATGCAATTAACCTTTTACAGATTTTGGCGCTGTTTGTGGCGATTCTGATCATCATG 782
DB 239 CACTGCATTGATCTCTTCTTAGATTTCATTCTGCTTTCAGAAAACTCATGATGATCTG 298
QY 783 TTAAGAATGCATCTGAGAGGAGGAGAGAGAGAA 817
DB 299 GCCATGAATGAAGGATGAAGAGAGAGAGAGAA 333

RESULT 12
ABO59227/c
ID ABO59227 standard; cDNA; 595 BP.
AC ABO59227;
XX
XX
XX 02-AUG-2002 (first entry)
XX
XX Human colon cancer related nucleotide sequence SEQ ID NO:2922.
XX
XX Human; colon cancer; cancer; tissue profiling; forensic; mapping;
XX genetic analysis; diagnostic; antisense therapy; gene; ss.
XX
XX Homo sapiens.
XX OS
XX WO200229086-A2.
XX
XX 11-APR-2002.
XX
XX 02-OCT-2001; 2001WO-US30732.
XX
XX 02-OCT-2000; 2000US-237271P.
XX
XX (FARB) BAYER CORP.
XX
XX Burgess C, Astle JH, Carroll E, Catino TJ, Dwivedi P, Molino GA;
XX Thiagalingam A, Lewis ME;
XX WPI; 2002-426115/45.
XX
XX New isolated nucleic acid that is differentially expressed in cancer
XX tissues useful for determining the presence of colon cancer in a cell
XX or tissue type, and in antisense therapy .
XX
XX Claim 1; Fig 1; 796pp; English.
XX
XX ABO56306 to ABO60787 represent isolated nucleic acids (I) differentially
XX expressed in cancer tissues. ABB78993 to ABB79004 represent proteins
XX encoded by the ABO60776 to ABO60787 nucleic acid sequences. (I) can be
XX used in antisense therapy. An antibody immunoreactive with a polypeptide
XX encoded by (I) is useful for detecting cancer in a patient sample, and
XX for detecting the presence or absence of a polynucleotide encoded by a
XX nucleic acid which hybridises to (I) in a cell. A probe/primer derived
XX from (I) can be used for determining the presence of a nucleic acid which
XX hybridises to (I), and for determining the phenotype of cells in a sample
XX of cells from a patient. (I) is useful for determining the presence of
XX colon cancer in a cell or tissue type, for determining the presence or
XX state of other type of cancer, in antisense therapy, to generate
XX macroarrays on a solid surface, to identify a chromosome on which the
XX corresponding gene resides, and in tissue profiling, forensic, genetic
XX analysis, mapping and diagnostic applications. (I) can be used to raise
XX antibodies, and to screen for peptide analogues and antagonists.
XX
XX Sequence 595 BP; 180 A; 124 C; 130 G; 155 T; 6 other;
XX
XX Query Match 7.2%; Score 74; DB 24; Length 595;
XX Best Local Similarity 58.0%; Pred. No. 2.9e-11;
XX Matches 131; Conservative 0; Mismatches 95; Indels 0; Gaps 0;
XX
XX 592 TTTTGGGTGCTCCATGGCTGTTTCAAGTTTCACTTTATTTGGACTCTTGCTGTTG 651
XX
XX 368 TTTTCTTTGGATCCATTTGGCTTTTCCAGGCAACCTGTATGTGGACTGGTGTCTATG 309
XX
XX 652 TGGGCTACATCGCTTTTGACCCCAAGAAATTTATTGAGAAGGCTCCTTGGGTGATATGG 711
XX
XX 308 GTGGCTTCGCTCTTTTGTATCTCACTATTATTGAAAGGCGCAACATGAGATCAAG 249
XX
XX 712 ATTACGTTAAGCATGATGACCCCTTTTACAGATTTTGGCGCTGTTTGTGGCGATTTC 771
XX
XX 248 ATTATATCTGGCACTGCAATGATCTCTTCTTAGATTTTCTTACTGTCTCTGAGAAATCA 189
XX
XX 772 TGATCATCATGTTTAAAGATGCAATCTGACAGGAAGAGAGAGAA 817
XX
XX

Db 188 TGATGATCTCTGCCATGATGAATGAAGAAGGATAGAGAAGAGAGAA 143
RESULT 13
AAV86028
ID AAV86028 standard; cDNA; 520 BP.
AC AAV86028;
XX
XX 27-APR-1999 (first entry)
XX
XX EST clone B115.
XX
XX Expressed sequence tag; secreted protein; haematopoiesis regulator;
XX tissue growth; activin; inhibin; tumour invasion suppressor; EST; human;
XX chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
XX receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
XX
XX Homo sapiens.
XX OS
XX WO9845435-A2.
XX
XX 15-OCT-1998.
XX
XX 10-APR-1998; 98WO-US05954.
XX
XX 10-APR-1997; 97US-0835913.
XX
XX (GEMY) GENETICS INST INC.
XX
XX Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
XX Racie LA, Spaulding V, Treacy M;
XX WPI; 1999-070076/06.
XX
XX New polynucleotides encoding human secreted proteins - derived from
XX e.g. human blood, kidney, foetal lung, placenta, testes, brain,
XX ovary, pituitary, retina and colon cDNA libraries
XX
XX Claim 1; Page 94; 633pp; English.
XX
XX This sequence represents an expressed sequence tag (EST), and is a
XX polynucleotide of the invention. The polynucleotides of the invention are
XX all secreted EST sequences isolated from a variety of human tissue
XX sources. The EST sequences and proteins encoded by them are predicted to
XX have useful biological activities which would make them suitable for
XX treating, preventing or ameliorating medical conditions in humans and
XX animals, although no supporting data is given. Suggested activities
XX include nutritional activity, immune stimulating or suppressing activity,
XX haematopoiesis regulating activity, tissue growth activity, haemostatic
XX activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity, receptor/ligand activity, anti-inflammatory
XX activity, cadherin/tumour invasion suppressor activity, tumour inhibition
XX activity. The EST sequences are also stated to be useful for gene
XX therapy.
XX
XX Sequence 520 BP; 103 A; 140 C; 123 G; 154 T; 0 other;
XX
XX Query Match 7.0%; Score 72; DB 20; Length 520;
XX Best Local Similarity 51.1%; Pred. No. 1e-10;
XX Matches 227; Conservative 0; Mismatches 205; Indels 12; Gaps 2;
XX
XX 144 TATGATTTCTCAAAAACCTCCGCCAGATCTGCCTCTCGTTCAAACTCATCTCAAGCAG 203
XX
XX 53 TTTGATGGCTTTTAAATTTTCTCATATAACCCCGTCACGACGACGACCTGAAGAAG 112
XX
XX 204 GTGTACCTTACGCTATGCTGTGCTTTAGTGGCATCGGCTCTGGGGCTTACCTTCA---- 259
XX
XX 113 GTCTATGCAAGTTTGGCTTTGATGTTTGGCGGCTCTGACGGGCTATGTCATATG 172
XX
XX 260 --CATTCTATGGAATATCGGTGGCTCTCTCACAACATGCTTGCATGGGAGCAGTGG 317
XX
XX 173 GTCACTCATTTTCATTCAGGCTGGCTCTGCTGTGCTGGGCTCCCTGATTTGATGATT 232
XX

CC antibodies, and to screen for peptide analogues and antagonists.
XX
SQ Sequence 689 BP; 204 A; 157 C; 154 G; 158 T; 16 other;
Query Match 6.6%; Score 68.4; DB 24; Length 689;
Best Local Similarity 59.3%; Pred. No. 1.3e-09;
Matches 134; Conservative 0; Mismatches 91; Indels 1; Gaps 1;
QY 592 TTTTGGTGGTTCATGGCTGTTTCAAGTTTGAGTTTGATTTTGGACTCTTGGTGTG 651
Db 349 TTTTCTTTGGATCCATTGGCTTTCCAGGCAACCTGATGTGGAGCTGGTGGT-CATG 291
QY 652 TGGGTACATCGTCTTTGACACCCAGAAATTTATGAGAGGCTCACTTGGGTGATATG 711
Db 290 TGGGCTTCGTCTTTTGGATCTCACTCATTTATGAAAGGCCGCAACATGAGATCAAG 231
QY 712 ATTACGTTAAGCATGCATTCACCCCTTTTCACAGATTTTGGCGCTGTTTGTGCGGATTC 771
Db 230 ATTATATCTGGCACTGCATTTGATCTCTTCTTAGATTTTCACTGCTTTCAGAAAACTCA 171
QY 772 TGATCATCATGTTAAGAAATGCATCTCGAAGGAGGAGAGAGAGAA 817
Db 170 TGATGATCTCGCCATGAATGAAAGGATAAGAGAGAGAGAGAGAA 125
RESULT 15
ABQ58023/C
ID ABQ58023 standard; cDNA; 506 BP.
XX
AC ABQ58023;
XX
DT 02-AUG-2002 (first entry)
XX
DE Human colon cancer related nucleotide sequence SEQ ID NO:1718.
XX
KW Human; colon cancer; cancer; tissue profiling; forensic; mapping;
KW genetic analysis; diagnostic; antisense therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200229086-A2.
XX
PD 11-APR-2002.
XX
PF 02-OCT-2001; 2001WO-US30732.
XX
PR 02-OCT-2000; 2000US-237271P.
XX
PA (FARB) BAYER CORP.
XX
PI Burgess C, Astle JH, Carroll E, Catino TJ, Dwivedi P, Molino GA;
PI Thiagalingam A, Lewis ME;
XX
WPI; 2002-426115/45.
XX
PT New isolated nucleic acid that is differentially expressed in cancer
PT tissues useful for determining the presence of colon cancer in a cell
PT or tissue type, and in antisense therapy -
XX
PS Claim 1; Fig 1; 796pp; English.
XX
CC ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially
CC expressed in cancer tissues. ABB78993 to ABB79004 represent proteins
CC encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be
CC used in antisense therapy. An antibody immunoreactive with a polypeptide
CC encoded by (I) is useful for detecting cancer in a patient sample, and
CC for detecting the presence or absence of a polynucleotide encoded by a
CC nucleic acid which hybridizes to (I) in a cell. A probe/primer derived
CC from (I) can be used for determining the presence of a nucleic acid which
CC hybridizes to (I), and for determining the phenotype of cells in a sample
CC of cells from a patient. (I) is useful for determining the presence of
CC colon cancer in a cell or tissue type, for determining the presence or
CC state of other type of cancer, in antisense therapy, to generate
CC analysis, mapping and diagnostic applications. (I) can be used to raise

318 TGGCTTCTCTCAGTCTCTCTTATCAAGAG-----CAAAAAGGGTGGCTCTCTCTGATG 371
233 TGGCTGATGGCAACACCTCATAGCCATGAACAAAGAGACTGGACATCTTGCT 292
372 CGAGCTGCACATTTTGAAGGCGCTCTATTGGTCTCTGATGTGAGCTGGGCATTAATTC 431
293 GGATTGCAATCTTACAGGAGTTGGCGCTGGCCCTGCCCTGGAGTTTGTATGTCTGTC 352
432 GATCAGCAATGTGTTGGCGCTTTTGTAGTTGCTGCTGGTTTGGTGTCTTCTCA 491
353 AACCACAGCATCTTCCACATGCTTTATGGGACGGCAATGATCTTTACTGCTTACC 412
492 GCTGCTGCCATGTTGGCAAGGCGCAGGAGTACTTGTACCTCGGGGCGCTTCTTTCATCT 551
413 CTCAGTGCACTATATGCCAGGCGCGGCTACCTCTTCTGGGAGGTATCTTGATGTC 472
552 GCGCTCCCTTCTCTTCTGTTG 575
473 GCGCTGAGCTTGTGCTTTGTCG 496
RESULT 14
ABQ60318/C
ID ABQ60318 standard; cDNA; 689 BP.
XX
AC ABQ60318;
XX
DT 02-AUG-2002 (first entry)
XX
DE Human colon cancer related nucleotide sequence SEQ ID NO:4013.
XX
KW Human; colon cancer; cancer; tissue profiling; forensic; mapping;
KW genetic analysis; diagnostic; antisense therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200229086-A2.
XX
PD 11-APR-2002.
XX
PF 02-OCT-2001; 2001WO-US30732.
XX
PR 02-OCT-2000; 2000US-237271P.
XX
PA (FARB) BAYER CORP.
XX
PI Burgess C, Astle JH, Carroll E, Catino TJ, Dwivedi P, Molino GA;
PI Thiagalingam A, Lewis ME;
XX
WPI; 2002-426115/45.
XX
PT New isolated nucleic acid that is differentially expressed in cancer
PT tissues useful for determining the presence of colon cancer in a cell
PT or tissue type, and in antisense therapy -
XX
PS Claim 1; Fig 1; 796pp; English.
XX
CC ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially
CC expressed in cancer tissues. ABB78993 to ABB79004 represent proteins
CC encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be
CC used in antisense therapy. An antibody immunoreactive with a polypeptide
CC encoded by (I) is useful for detecting cancer in a patient sample, and
CC for detecting the presence or absence of a polynucleotide encoded by a
CC nucleic acid which hybridizes to (I) in a cell. A probe/primer derived
CC from (I) can be used for determining the presence of a nucleic acid which
CC hybridizes to (I), and for determining the phenotype of cells in a sample
CC of cells from a patient. (I) is useful for determining the presence of
CC colon cancer in a cell or tissue type, for determining the presence or
CC state of other type of cancer, in antisense therapy, to generate
CC macroarrays on a solid surface, to identify a chromosome on which the
CC corresponding gene resides, and in tissue profiling, forensics, genetic
CC analysis, mapping and diagnostic applications. (I) can be used to raise

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OM nucleic - nucleic search, using sw model

Run on: May 25, 2003, 10:14:23 ; Search time 75 Seconds
(without alignments)
4228.050 Million cell updates/sec

Title: US-09-955-526-3
Perfect score: 1034
Sequence: 1 ggcgaacataacattgtct.....ataaggaaagtctctgtga 1034

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/prodata/2/ina/5A_COMB.seq: *
2: /cgn2_6/prodata/2/ina/5B_COMB.seq: *
3: /cgn2_6/prodata/2/ina/6A_COMB.seq: *
4: /cgn2_6/prodata/2/ina/6B_COMB.seq: *
5: /cgn2_6/prodata/2/ina/PCUS_COMB.seq: *
6: /cgn2_6/prodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	221.2	21.4	884	4	US-09-325-932A-43
2	219.2	21.2	527	4	US-09-325-932A-44
3	122	11.8	2634	2	US-08-818-514-1
c 4	122	11.8	2634	2	US-08-818-514-2
5	122	11.8	2634	3	US-09-115-934A-1
c 6	122	11.8	2634	3	US-09-115-934A-2
7	48.8	4.7	7218	1	US-08-232-463-14
c 8	40.8	3.9	2296	2	US-08-899-336-2
9	36.8	3.6	601	4	US-09-385-982-231
10	34.6	3.3	2169	3	US-08-981-803-14
c 11	34.6	3.3	2169	3	US-08-981-803-28
12	34.6	3.3	2169	4	US-08-983-440-14
c 13	34.6	3.3	2169	4	US-08-983-440-28
14	34.6	3.3	11478	3	US-08-981-803-29
15	34.6	3.3	11478	4	US-08-983-440-29
c 16	34.4	3.3	112132	4	US-09-741-150-3
c 17	33.6	3.2	6755	3	US-08-911-999-4
18	33.4	3.2	3717	1	US-08-026-1388-7
c 19	33.2	3.2	1070	4	US-09-718-841-3
c 20	33.2	3.2	1070	4	US-09-718-810-3
c 21	33.2	3.2	1512	2	US-08-909-965C-8
c 22	33.2	3.2	1689	4	US-09-718-841-1
c 23	33.2	3.2	1689	4	US-09-718-810-1
c 24	33	3.2	688	4	US-08-998-416-915
25	32.8	3.2	2943	2	US-08-788-892-1
26	32.8	3.2	2943	2	US-08-340-475-1
27	32.4	3.1	5433	3	US-08-929-329-1

c 28	32	3.1	176373	3	US-09-128-155-17	Sequence 17, Appl
29	31.6	3.1	1418	4	US-09-111-470-7	Sequence 7, Appl
c 30	31.6	3.1	8789	1	US-08-328-254-5	Sequence 5, Appl
31	31.2	3.0	692	1	US-08-465-293A-1	Sequence 1, Appl
32	31.2	3.0	692	2	US-08-463-387A-1	Sequence 1, Appl
33	31.2	3.0	692	3	US-09-102-977-1	Sequence 1, Appl
34	31.2	3.0	692	4	US-09-034-088A-1	Sequence 1, Appl
c 35	31.2	3.0	2343	4	US-09-643-597-368	Sequence 368, App
c 36	31.2	3.0	4453	4	US-09-146-053-5	Sequence 5, Appl
c 37	31	3.0	6433	4	US-08-927-219-128	Sequence 128, App
38	31	3.0	38584	4	US-09-453-702B-50	Sequence 50, Appl
c 39	30.8	3.0	2254	4	US-09-138-277C-2	Sequence 2, Appl
40	30.8	3.0	3997	3	US-08-947-823-2	Sequence 2, Appl
41	30.8	3.0	51952	3	US-08-947-823-1	Sequence 4, Appl
42	30.6	3.0	982	3	US-08-725-532A-4	Sequence 4, Appl
c 43	30.6	3.0	1679	2	US-08-708-958-5	Sequence 5, Appl
c 44	30.6	3.0	72604	4	US-09-288-392-7	Sequence 7, Appl
c 45	30.6	3.0	72604	4	US-09-657-474-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-325-932A-43
; Sequence 43, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; FILE OF INVENTION: Death and their use in the modification of forestry plant devel
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325.932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 884
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-325-932A-43

Query Match	21.4%	Score	221.2	DB	4	Length	884
Best Local Similarity	60.6%	Pred	No. 1.4e-52				
Matches	383	Conservative	0	Mismatches	243	Indels	6
Gaps	1						
Qy	203	GGGTACCTTACGCTATGCTGTCTTACTGGCATGGCTGCTGGGCTTACCTTCACAT	262				
Db	4	GGTTTATTTGCTTAGCTGTGCTTAAACAGCAGCGATCGGTGTTTATTTGCATCT	63				
Qy	263	TCTATGGAATATCGTGGCTCTCTACACAAATGCTGTCATGGGAAGCATGGTGGCT	322				
Db	64	TCTTTGAATATTTGGAGGGCTCTCTACGGGGCTCGCTTGCATTTGTTTGTAAATCGGCT	123				
Qy	323	TCTCTACGCTCTCTCTT-----ATCAAGAGCAAAAAGGTTGCTTCTTGTATGGCAGC	376				
Db	124	CTTATCGTCCCTTACTTCTTCGAAACAATGAGGTAAGAGAGCTGGCTCTCTGGCAGC	183				
Qy	377	TGCATTTTGAAGGGCCCTTATTCGCTCTGATGAGCTGGCATTACTTCGATCC	436				
Db	184	TGCTCGTTCAAGGAGAGTACTCTGGGACCGCTCATCGACGGGTCATTATATTGATCTC	243				
Qy	437	AAGCATTTGCTTTGGGGCTTTTGTAGGTTGTCTGTGTTTGTGTTGCTCTCAGCTGC	496				
Db	244	CAGTATCTGGTGGTGGTTTGTGGACCTCTTTGGCTTGGCTTGTGTTTGGCAGC	303				
Qy	497	TGCCATTTGGCAAGCGCAGGAGTACTTGTACCTCGGGGCTCTTTCATCTTGGCT	556				
Db	304	AGCAATCACAGCCAGGAGCGGAATACCTATTTTGGAGGATATTGGGCTCGGGAAT	363				
Qy	557	CTCCTCTCTCTCTGTTGGTTGCATTTTGCATCTCTCTTGTGTTGTTCCATGCTGTTTT	616				

Db 520 GGCCTGAGCTTGTCTTTGCTCTCCCTGGGAAAT---GTTTCTTTTGGATCAATTTGG 576
2Y 612 GTTTTCAAGTTTGAGTCTTATTTGGACTCTTGTGTTGGGCTACATCGTCTTGAC 871
Db 577 CTTTTCCAGGAAACCTGTATGTGGACTGTGTGTCATGTGTGCTTGCCTTTTGTAT 636
2Y 672 ACCCAAGAAATTAATTGAGAAGGCTCACCTTGGTGATATGGATTACGTTAAGCATGCAATTG 731
Db 637 ACTCAACTCATTAATTGAAAGGCGCAACATGGAGATCAAGATTATATCTGGCACTGCATT 696
2Y 732 ACCCTTTTACAGATTTTGGCGCTGTTTGTGCGGATCTTGATCATCATGTTTAAAGAAAT 791
Db 697 GATCTCTTTAGATTTTCAATTAATCTCTCTCAGAAACTCATGATGATCTCTGGCCATGAAT 756
2Y 792 GCATCTGAGAAGGAAAGAGAAGAA 817
Db 757 GAAAGGATAAGAAAGAGAAGAA 782

RESULT 4

JS-08-818-514-2/c
; Sequence 2, Application US/0818514
; Patent No. 5837838
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Xu, Qunli
; TITLE OF INVENTION: BAX Inhibitor Proteins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell & Flores
; CITY: San Diego
; STREET: 4370 La Jolla Village Drive, Suite 700
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,514
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2446
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2634 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-818-514-2

Query Match 11.8%; Score 122; DB 2; Length 2634;

Best Local Similarity 51.9%; Pred. No. 1.4e-24;

Matches 356; Conservative 0; Mismatches 315; Indels 15; Gaps 3;

QY 144 TATGATCTCTCAAAATCTCGCGAGATCTCACTCTCTGTTCAAATCATCTCAAGCAG 203
Db 2535 TTTGATGCGCTTTTAAATTTTCTCATATAACCCGTCACGCGAGCACCTGAAGA 2476
QY 204 GTGTACCTTACGCTATGCTGTTAGTGCGATCGGTGCTGGGGCTTACCTCA--- 259
Db 2475 GCTATGGAAGTTTGGCCCTTTGATGTTTGGCGGCTGAGGGGCTATGTCATATG 2416
QY 260 --CATTTATGAATATCGGTGGCTCTCAACAATGGCTTGCATGGGAAGCATGGTG 317

Db 2415 GTCACTCATTTTCAATTCAGGCTGGCCTGCTGCTGCTTGGGCTCCCTGATATGATGATT 2356
QY 318 TGGCTTCTTCACAGCTCCTCCTTATCAAGG-----CAAAAAGGGTGGCTCTTCGANG 371
Db 2355 TGGTGATGGCAACACTTCATAGCCATGAACGACAGAAAACCTGGACTTCTTGCT 2296
QY 372 GCAGCTGCACCTTTTGAAGGCGCTCTATTTGGTCTCTCTGATTTAGCTGGGCATTAACCTTC 431
Db 2295 GGATTTGCAATTCCTTACAGGAATTTGGCCTGGGCTGCGCTGGAGTTTGTATTTGCTGTC 2236
QY 432 GATCCAGCAATTTGTTGGCGCTTTTGTAGGTTTGTGCTGCTGCTTTTGGTGGCTTCTCA 491
Db 2235 AACCCAGCATCTTCCCACTGCTTTTCATGGCAGGCAAGATCTTTACCTGCTTCAAC 2176
QY 492 GCTGCTGCCATTTGGCAAGCGCAGGAGTACTTTGTAOCTCGGGGGCCTTTCTTCATCT 551
Db 2175 CTCAGTGCACCTCTATGCCAGGCGCGTAGCTACCTCTTCTCGGAGGTATCTTGATGTCA 2116
QY 552 GCGCTCTCCCTCTCTTCTGTTGCACTTTGCACTTCCATCTCCATTTTGGTGGTCCATGGCT 611
Db 2115 GCGCTGAGCTTGTGCTTTTGTCTTCCCTGGGAAAT---GTTTCTTTGGATCCATTGG 2059
QY 612 GTTTTCAAGTTTGAAGTTTGTATTTTGGACTCTTGGTGTGTTGTGGGCTACATCGTCTTTGAC 671
Db 2058 CTTTTCCAGGCAACCTGTATGTGGACTGGTGTGTCATGTGTGCTTCTGCTTTTGTAT 1999
QY 672 ACCCAAGAAATTTAGAGAGGCTCACTTGGTGTGATATGATTAAGCATGCAATTG 731
Db 1998 ACTCAACTCATTAATTGAAAAGGCGCAACATGGAGATCAAGATTATATCTGGCACTGCATT 1939
QY 732 ACCCTTTTACAGATTTTGGCGCTGTTTGTGGGATCTGATCATCATGTTTAAAGAAAT 791
Db 1938 GATCTCTTTAGATTTTCAATTAATCTGCTTTCAGAAAACATCATGATGATCTCGGCAAT 1879
QY 792 GCATCTGAGAAGGAAAGAGAAGAA 817
Db 1878 GAAAGGATAGAAAGAGAAGAA 1853

RESULT 5

US-09-115-934A-1
; Sequence 1, Application US/09115934A
; Patent No. 6130317
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Xu, Qunli
; TITLE OF INVENTION: BAX Inhibitor Proteins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/115,934A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/818,514
; FILING DATE: 14-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001

STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
Zip: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,934A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/818,514
FILING DATE: 14-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 3209
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2634 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-115-934A-2

TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2634 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-115-934A-1

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100	TTTGATGCGCTTTTAAATTTCTCATATAACCCGCTCAACGACGACGACCTGAAGAAG	159
204	GTGTACCTTACGCTATCTGCTTTTAGTGGCATCGGCTCGTGGGCTTACCTTCA	259
160	GTCTATGCAAGTTTGGCCCTTTGATGTTTGTGGGCGCTGACGAGCCCTATGTCCATATG	219
260	--CATTCTATGGAATATCGGTGGCTCCTCACAACTATGCTTGCATGGGAAGCATGGTG	317
220	GTCACTCATTTCACTAGGCTGGCCCTGCTCTGCTTGGCTCCCTGATATTGATGATT	279
318	TGGCTTCTCAGCTCTCTCTTATCAAGG-----CAAAAAGGCTGCTTCTCTGATG	371
280	TGGCTGATGGCAACACCTATAGCCATGAACCTGAACAGAAAAAATGGGACTTCTTGTCT	339
372	GCAGCTGCACCTTTTGAAGCGCCTCTATTGCTCTCTGATTCAGCTGGGCTTAACTTC	431
340	GGATTGCAATTCCTTACAGGAATTTGGCTGGCCCTGCGCTGGAGTTTGTATTGCTGTC	399
432	GATCAAGCATGTTTGGGCTTTTGTAGGTTGTGCTGTGCTTTTGGTGTCTTCTCA	491
400	AACCCAGCATCTCCACCTGCTTTTCATGGGACGCGCAATGATCTTTACCTGCTTCAC	459
492	GCTGCTGCATGTTGGAAGCGCAGGAGTACTTGTACCTCGGGGCTTCTTTCATCT	551
460	CTCAGTGCACTATATGCGAGCGCCGCTAGTACCTCTTCTGGAGGATCTTGTATGICA	519
552	GGGCTCTCCCTTCTCTGCTGCTTGTGATCTTGCATCTCCATTTTGGTGGTTCATGGCT	611
520	GCCCTGAGCTTGTGCTTTTGTCTTCCCTGGGAAT---GTTTTCTTGGATCCATTGG	576
612	GTTTTCAAGTTGTAGTTGATTTTGGACTCTTGTGTTTGTGGCTACATGCTCTTGAC	671
577	CTTTTCCAGCAACCTGTATGTGGGACTGGTGGTCAATGTGCTTCTCTTTTGTAT	636
672	ACCCAAGAAATATTGAGAGGCTCACTGGGTGATGATGATTAAGCATGCAATG	731
637	ACTCACTCATTTTGAAGGCGCAACATGGAGATCAAGATTATATCTGGCACTGCAAT	696
732	ACCCCTTTCAGATTTTGGGCTGTTTGTGGGATTTCTGATCATCATGTTTAAAGAAAT	791
697	GATCTCTTCTTATGATTTCACTTCTCTTCAAAAACCTCATGATGATCTGGCCATGAAT	756
792	GCATCTGAGAAGGAGAGAGAGAA 817	
757	GAAGAAGGATAAGAAGAGAGAA 782	

RESULT 6

US-09-115-934A-2/c

Sequence 2, Application US/09115934A

Patent No. 6130317

GENERAL INFORMATION:

APPLICANT: Reed, John C.

APPLICANT: Xu, Qunli

TITLE OF INVENTION: BAX Inhibitor Proteins

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

US-08-899-336-2

Query Match	3.9%	Score 40.8;	DB 2;	Length 2296;
Best Local Similarity	52.3%;	Pred. No. 0.07;		

Db 1743 GAGTTTATGATTAAGTTCATCTTATGATATGATTAACATCTTATTATAGATGCATATA 1684
QY 810 AAGAAGAAGAGGAGGAGAACTAGATTG 838
Db 1683 AATAGCTAATGATAGACATTGACATTG 1655

RESULT 12
US-08-983-440-14
; Sequence 14, Application US/08983440
; Patent No. 6232122
; GENERAL INFORMATION:
; APPLICANT: POULSEN, Peter
; TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION
; FILE REFERENCE: 674509-2003
; CURRENT APPLICATION NUMBER: US/08/983,440
; CURRENT FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 9514437.4
; EARLIER FILING DATE: 1995-07-14
; EARLIER APPLICATION NUMBER: PCT/EP96/03053
; EARLIER FILING DATE: 1996-07-12
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: Solanum tuberosum
US-08-983-440-14

Query Match 3.3%; Score 34.6; DB 4; Length 2169;
Best Local Similarity 47.8%; Pred. No. 3.7;
Matches 100; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 630 TATTTGGACTCTTGGTGTGTTGGGCTACATCGTCTTTGACACCCCAAGAAATTTAG 689
Db 307 TATTTGTTCTCTTATTATTATATCATACATACATTATTACAAGGAAAGACAAGTACA 366
QY 690 AAGGCTCATTGGGTGATGATGATTAAGCTTAAGCATGATGACCCCTTTTCACAGATTTT 749
Db 367 CAGATCTTAACGTTTATGTTCAATCACTTTTGGAGGCAATGACAGGTACCAAAATTTT 426
QY 750 GCGCTGTTTTGTGCGGATTCATCATCTTAAAGATGCTGAGAGGAAGAG 809
Db 427 GAGTTTATGATTAAGTTCAATCTTAGAATATGAATTTAAATCTATTATAGATGCATATA 486
QY 810 AAGAAGAAGAGGAGGAGAACTAGATTG 838
Db 487 AATAGCTAATGATAGACATTGACATTG 515

RESULT 13
US-08-983-440-28/c
; Sequence 28, Application US/08983440
; Patent No. 6232122
; GENERAL INFORMATION:
; APPLICANT: POULSEN, Peter
; TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION
; FILE REFERENCE: 674509-2003
; CURRENT APPLICATION NUMBER: US/08/983,440
; CURRENT FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 9514437.4
; EARLIER FILING DATE: 1995-07-14
; EARLIER APPLICATION NUMBER: PCT/EP96/03053
; EARLIER FILING DATE: 1996-07-12
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 28
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: Solanum tuberosum
US-08-983-440-28

Query Match 3.3%; Score 34.6; DB 4; Length 2169;
Best Local Similarity 47.8%; Pred. No. 3.7;
Matches 100; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 630 TATTTGGACTCTTGGTGTGTTGGGCTACATCGTCTTTGACACCCCAAGAAATTTAG 689
Db 307 TATTTGTTCTCTTATTATTATATCATACATACATTATTACAAGGAAAGACAAGTACA 366
QY 690 AAGGCTCATTGGGTGATGATGATTAAGCTTAAGCATGATGACCCCTTTTCACAGATTTT 749
Db 367 CAGATCTTAACGTTTATGTTCAATCACTTTTGGAGGCAATGACAGGTACCAAAATTTT 426
QY 750 GCGCTGTTTTGTGCGGATTCATCATCTTAAAGATGCTGAGAGGAAGAG 809
Db 427 GAGTTTATGATTAAGTTCAATCTTAGAATATGAATTTAAATCTATTATAGATGCATATA 486
QY 810 AAGAAGAAGAGGAGGAGAACTAGATTG 838
Db 487 AATAGCTAATGATAGACATTGACATTG 515

RESULT 14
US-08-981-803-29
; Sequence 29, Application US/08981803
; Patent No. 6147279
; GENERAL INFORMATION:
; APPLICANT: POULSEN, PETER
; TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION
; FILE REFERENCE: 674509-2004
; CURRENT APPLICATION NUMBER: US/08/981,803
; CURRENT FILING DATE: 1997-04-17
; EARLIER APPLICATION NUMBER: PCT/EP96/03052
; EARLIER FILING DATE: 1996-07-12
; EARLIER APPLICATION NUMBER: 9514435.8
; EARLIER FILING DATE: 1995-07-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 29
; LENGTH: 11478
; TYPE: DNA
; ORGANISM: Solanum tuberosum
US-08-981-803-29

Query Match 3.3%; Score 34.6; DB 3; Length 11478;
Best Local Similarity 47.8%; Pred. No. 7.5; 109; Indels 0; Gaps 0;
Matches 100; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 630 TATTTGGACTCTTGGTGTGTTGGGCTACATCGTCTTTGACACCCCAAGAAATTTAG 689
Db 307 TATTTGTTCTCTTATTATTATATCATACATACATTATTACAAGGAAAGACAAGTACA 366
QY 690 AAGGCTCATTGGGTGATGATGATTAAGCTTAAGCATGATGACCCCTTTTCACAGATTTT 749
Db 367 CAGATCTTAACGTTTATGTTCAATCACTTTTGGAGGCAATGACAGGTACCAAAATTTT 426
QY 750 GCGCTGTTTTGTGCGGATTCATCATCTTAAAGATGCTGAGAGGAAGAG 809
Db 427 GAGTTTATGATTAAGTTCAATCTTAGAATATGAATTTAAATCTATTATAGATGCATATA 486
QY 810 AAGAAGAAGAGGAGGAGAACTAGATTG 838
Db 487 AATAGCTAATGATAGACATTGACATTG 515

RESULT 15
US-08-983-440-29
; Sequence 29, Application US/08983440
; Patent No. 6232122
; GENERAL INFORMATION:
; APPLICANT: POULSEN, Peter
; TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION
; FILE REFERENCE: 674509-2003
; CURRENT APPLICATION NUMBER: US/08/983,440

Query Match 3.3%; Score 34.6; DB 4; Length 2169;
Best Local Similarity 47.8%; Pred. No. 3.7;
Matches 100; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 630 TATTTGGACTCTTGGTGTGTTGGGCTACATCGTCTTTGACACCCCAAGAAATTTAG 689
Db 1863 TATTTGTTCTCTTATTATTATATCATACATACATTATTACAAGGAAAGACAAGTACA 1804
QY 690 AAGGCTCATTGGGTGATGATGATTAAGCTTAAGCATGATGACCCCTTTTCACAGATTTT 749
Db 1803 CAGATCTTAACGTTTATGTTCAATCACTTTTGGAGGCAATGACAGGTACCAAAATTTT 1744
QY 750 GCGCTGTTTTGTGCGGATTCATCATCTTAAAGATGCTGAGAGGAAGAG 809
Db 1743 GAGTTTATGATTAAGTTCAATCTTAGAATATGAATTTAAATCTATTATAGATGCATATA 1684
QY 810 AAGAAGAAGAGGAGGAGAACTAGATTG 838
Db 1683 AATAGCTAATGATAGACATTGACATTG 1655

RESULT 14
US-08-981-803-29
; Sequence 29, Application US/08981803
; Patent No. 6147279
; GENERAL INFORMATION:
; APPLICANT: POULSEN, PETER
; TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION
; FILE REFERENCE: 674509-2004
; CURRENT APPLICATION NUMBER: US/08/981,803
; CURRENT FILING DATE: 1997-04-17
; EARLIER APPLICATION NUMBER: PCT/EP96/03052
; EARLIER FILING DATE: 1996-07-12
; EARLIER APPLICATION NUMBER: 9514435.8
; EARLIER FILING DATE: 1995-07-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 29
; LENGTH: 11478
; TYPE: DNA
; ORGANISM: Solanum tuberosum
US-08-981-803-29

Query Match 3.3%; Score 34.6; DB 3; Length 11478;
Best Local Similarity 47.8%; Pred. No. 7.5; 109; Indels 0; Gaps 0;
Matches 100; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 630 TATTTGGACTCTTGGTGTGTTGGGCTACATCGTCTTTGACACCCCAAGAAATTTAG 689
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QY 690 AAGGCTCATTGGGTGATGATGATTAAGCTTAAGCATGATGACCCCTTTTCACAGATTTT 749
Db 367 CAGATCTTAACGTTTATGTTCAATCACTTTTGGAGGCAATGACAGGTACCAAAATTTT 426
QY 750 GCGCTGTTTTGTGCGGATTCATCATCTTAAAGATGCTGAGAGGAAGAG 809
Db 427 GAGTTTATGATTAAGTTCAATCTTAGAATATGAATTTAAATCTATTATAGATGCATATA 486
QY 810 AAGAAGAAGAGGAGGAGAACTAGATTG 838
Db 487 AATAGCTAATGATAGACATTGACATTG 515

RESULT 15
US-08-983-440-29
; Sequence 29, Application US/08983440
; Patent No. 6232122
; GENERAL INFORMATION:
; APPLICANT: POULSEN, Peter
; TITLE OF INVENTION: INHIBITION OF GENE EXPRESSION
; FILE REFERENCE: 674509-2003
; CURRENT APPLICATION NUMBER: US/08/983,440

Search completed: May 25, 2003, 11:26:51
Job time : 90 secs

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 25, 2003, 11:00:18 ; Search time 165 Seconds
(without alignments)
8274.897 Million cell updates/sec

Title: US-09-955-526-3
Perfect score: 1034
Sequence: 1 gagcaacatacaattgtct.....ataaggaaagtctctgtga 1034

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 828747 seqs, 660231138 residues
Total number of hits satisfying chosen parameters: 1657494

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*
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3: /cgn2_6/ptodata/2/pubna/US05_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubna/US06_PUBCOMB.seq:*
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11: /cgn2_6/ptodata/2/pubna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	ID	Description
1	1033.99.9	1034	9	US-09-955-526-3	Sequence 3, Appli
2	429.41.5	735	9	US-10-167-015-15	Sequence 15, Appl
3	428.8	41.5	1009	US-09-770-445-223	Sequence 223, App
4	417.4	40.4	989	US-10-167-015-17	Sequence 17, Appl
5	411.39.7	1218	9	US-10-219-220-232	Sequence 232, App
6	314.4	30.4	1026	US-10-167-015-31	Sequence 31, Appl
7	312.30.2	957	9	US-10-167-015-1	Sequence 1, Appl
8	310.4	30.0	1138	US-10-167-015-33	Sequence 33, Appl
9	310.4	30.0	1139	US-10-167-015-5	Sequence 5, Appli
10	305.29.5	1026	9	US-10-167-015-3	Sequence 3, Appli
11	245.6	23.8	1102	US-10-219-220-231	Sequence 231, App
12	221.2	21.4	884	US-10-219-220-43	Sequence 43, Appl
13	219.2	21.2	527	US-10-219-220-44	Sequence 44, Appl
14	178.8	17.3	740	US-10-167-015-7	Sequence 7, Appl
15	172.8	17.2	308	US-10-167-015-22	Sequence 22, Appl
16	172.8	16.7	376	US-09-878-574-1827	Sequence 1827, Ap
17	157.8	15.3	234	US-10-167-015-19	Sequence 19, Appl
18	125.2	12.1	2922	US-09-925-302-73	Sequence 73, Appl
19	125.2	12.1	2994	US-10-044-090-356	Sequence 356, App

ALIGNMENTS

RESULT 1

US-09-955-526-3
; Sequence 3, Application US/09955526
; Publication No. US20030009785A1
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: Plant Cytoprotective Genes and Methods
; FILE REFERENCE: P-LJ 4868
; CURRENT APPLICATION NUMBER: US/09/955,526
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 09/661,014
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1034
; TYPE: DNA
; ORGANISM: Lycopodium esculentum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (87)...(830)
; NAME/KEY: misc feature
; LOCATION: (1)...(1034)
; OTHER INFORMATION: n = A,T,C or G
US-09-955-526-3

Query Match 99.9%; Score 1033; DB 9; Length 1034;
Best Local Similarity 100.0%; Pred. No. 3.2e-313;
Matches 1034; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGCAACATAACATTGTCTACGTTTCAGATAATATCTTGTCTCATTTTCAGTTCACAAA 60
Db 1 GAGCAACATAACATTGTCTACGTTTCAGATAATATCTTGTCTCATTTTCAGTTCACAAA 60
QY 61 ACTCGAAG 120
Db 61 ACTCGAAG 120
QY 121 CTGCTCTCGACCGCTGAGTTATGATTCTCTCAAAACTTCGCCAGATCTCACCTC 180
Db 121 CTGCTCTCGACCGCTGAGTTATGATTCTCTCAAAACTTCGCCAGATCTCACCTC 180

181 TCCTTCAAACTCATCTCAAGAGGTGACTTACGCTATGCTGTGCTTTAGTGGCATCGG 240
Db TCCTTCAAACTCATCTCAAGAGGTGACTTACGCTATGCTGTGCTTTAGTGGCATCGG 240
QY CTGCTGGGGCTTACCTTCAACATCTATGGAATATCGGTGGCCCTCTCAACAATGGCTT 300
Db CTGCTGGGGCTTACCTTCAACATCTATGGAATATCGGTGGCCCTCTCAACAATGGCTT 300
QY GCATGGGAAGCATGGTGTGCTTCTCTCAGCTCCCTCTTATCAAGAGCAAAAAGGGTGG 360
Db GCATGGGAAGCATGGTGTGCTTCTCTCAGCTCCCTCTTATCAAGAGCAAAAAGGGTGG 360
QY CTCTCTGTATGGCAGCTGCACATTTTGAAGGGCCCTCTATTTGGTCCCTGTATGAGCTGG 420
Db CTCTCTGTATGGCAGCTGCACATTTTGAAGGGCCCTCTATTTGGTCCCTGTATGAGCTGG 420
QY GCATTAACCTTCGATCCAAAGCATTTGCTTTGGGGCTTTTCTAGTGTGCTGTGTTTTTG 480
Db GCATTAACCTTCGATCCAAAGCATTTGCTTTGGGGCTTTTCTAGTGTGCTGTGTTTTTG 480
QY GTTGCTTCTCAGCTGTGCGCATGTTGGCAAGGCGCAGGAGTACTTGTACCTCGGGGGCC 540
Db GTTGCTTCTCAGCTGTGCGCATGTTGGCAAGGCGCAGGAGTACTTGTACCTCGGGGGCC 540
QY TTCTTTTCATCTGGGCTCTCCCTCTCTCTCTGTTGACATTTTGCATCCCTCATTTTGTG 600
Db TTCTTTTCATCTGGGCTCTCCCTCTCTCTCTGTTGACATTTTGCATCCCTCATTTTGTG 600
QY GTTCCATGCGTGTGTTTCAAGTTTGAAGTTGATTTTGGCACTCTGTTGTTGGGCTACA 660
Db GTTCCATGCGTGTGTTTCAAGTTTGAAGTTGATTTTGGCACTCTGTTGTTGGGCTACA 660
QY TCGTCTTTGACCCCAAGAAATTTGAGAGGCTCACCTTGGGTGATGATGATGATGATTA 720
Db TCGTCTTTGACCCCAAGAAATTTGAGAGGCTCACCTTGGGTGATGATGATGATGATTA 720
QY AGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Db AGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY TGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
Db TGTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY TCTCAACTTGTGTTTCCANAACCTCTCTGTTGTTTCACTGAAACCAAGCATGTTAATGTT 900
Db TCTCAACTTGTGTTTCCANAACCTCTCTGTTGTTTCACTGAAACCAAGCATGTTAATGTT 900
QY GATACCTGCTTACCTTTAGCATAGGCTGTGATGATGATGATGATGATGATGATGATGATG 960
Db GATACCTGCTTACCTTTAGCATAGGCTGTGATGATGATGATGATGATGATGATGATGATG 960
QY TGTGTGATGAGCATCTAGCCTTTTATCTTCTAAAGCTTTTCTTAAAGCTTTTCTTAAAG 1020
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QY 1021 AAAGTTCCTTGTGA 1034
Db 1021 AAAGTTCCTTGTGA 1034

RESULT 2

US-10-167-015-15
; Sequence 15, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use

; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 735
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(735)
; US-10-167-015-15

Query Match 41.5%; Score 429; DB 9; Length 735;
Best Local Similarity 74.5%; Pred. No. 7.1e-124;
Matches 540; Conservative 0; Mismatches 185; Indels 0; Gaps 0;

QY 107 CTTGCACTCGAATCTGCTCTCGCAACCGCTGGAGTTATGATTTCTCTCAAAACTTCGG 166
Db 9 CTTCAATTCCTTCTTCGATTCAGAGAACCGATGGAATACGATACCTCTCAAAACTTCGG 68
QY 167 CCAGATCTCACCTCTCGTTCAAACTCATCTCAAGCAGGTGACCTTACGCTATGCTGTGC 226
Db 69 TCAGATTTCTCCGGTCGTCAGAAATCACCTGAGCAGGTTTATTTACTCTGTGTTTTGC 128
QY 227 TTTAGTGGCATCGGCTGTGGGGCTTACCTTCAATCTATGGAATATCGGTGGCCCTCT 286
Db 129 CGTGTGTGCTCGGGCTGTGGGGCTTACCTTCAATCTCTTGAACATTTGGGGTTTTCT 188
QY 287 CACAAATATGCTTGCATGGAAGCATGTTGGCTTCTCTCAGCTCTCTCTTATCAAGA 346
Db 189 TACTACAGTGGCATGCAATGGGAAGCAGCTTTTGGTTACTCTCCACACCTCTTTTGAAGA 248
QY 347 GCAAAAAGGGTGGCTTCTGATGCGAGCTGCATTTTGAAGCGCCCTATTTGGTCC 406
Db 249 GAGGAAGAGGGTGAATTTGATGCGCGCATCACTGTTTCAAGGGTTCTCTATTTGGACC 308
QY 407 TCTGATGAGCTGGGGCATTAACCTTCGATCCAAAGCATTTGTTTGGCGCTTTTGTAGGTTG 466
Db 309 CTGTGATGATTTGGCTATTTATATGATCCAGCCCTTATCTTTAGTGCATTTTGGGAAC 368
QY 467 TGTGTGGTTTTGTTGTTCTCTCAGCTGTGCCATGTTGCAAGCGCCAGGAGTACTT 526
Db 369 AGCTTTGGGCTTTGCAATGCTTCTCAGGAGCAGCTTGGTTGCAAGGCGTAGGGAGTACCT 428
QY 527 GTACCTCGGGGGCTTTCTTTCATCTGGGCTCTCCCTTCTCTTCTGTTGCACTTTGCATC 586
Db 429 GTACCTGTGGGCTTGGTTTCTTCTGGATTGTCATCTCTCTGTTTGCATTTTGTCTTC 488
QY 587 CTCATTTTGTGGTTCAGGCTGTTTCAAGTTTGAAGTTGATTTTGTGACTTTGGT 646
Db 489 TCCATCTTTGGAGGCTCAACAGCTCTCTTTAAGTTTGAAGTTGATTTTGGGCTATTGGT 548
QY 647 GTTTGGGCTACATCGTCTTTGACACCCCAAGAAATTTTGAAGAGGCTCACTTGGGTGA 706
Db 549 GTTTGAGTTTACATTTGTAGTAGACACCCCAAGAAATAGTTGAGAGGSCACACTTGGGGA 608
QY 707 TATGGAATACGTTAAGCATGCAATGACCTTTTCAAGATTTTGGCGCTGTTTTGTGCG 766
Db 609 TCTGGACTATGTAAGCATGCCCTTGACCTTGTTTACCGATTTGGTCCGAGTTTTTGTCCG 668
QY 767 GATTTCTGATCATCATGTTAAGAAATGCACTCTGAGAGGAGAGAGAGAGAGAGAGAG 826
Db 669 GATTTCTGTTTATTTATGTTGAGAAATTCGACTGAGAGGATGAGAGAGAGAGAGAGAG 728
QY 827 AAAT 831
Db 729 AGATT 733

```

RESULT 3
JS-09-770-445-223
; Sequence 223, Application US/09770445
; Patent No. US20020023281A1
; GENERAL INFORMATION:
; APPLICANT: Gornach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krieker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE OF INVENTION: thaliana
; FILE REFERENCE: 2023US (PARA-012PRV)
; CURRENT APPLICATION NUMBER: US/09/770,445
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,472
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 223
; LENGTH: 1009
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-445-223

Query Match 41.5%; Score 428.8; DB 10; Length 1009;
Best Local Similarity 73.7%; Pred. No. le-123;
Matches 560; Conservative 0; Mismatches 137; Indels 3; Gaps 1

QY 72 AAGAAGAAGAACATGAAGGTTTCACATCGTTTCTCGACTCGCAATCTGCCTCTCGC 131
DB 23 AAAAAAACAACAATGATGCGTTCTTCTTCCTTCCTCGATCTCAACCTG---GTAGC 79
QY 132 AACCGCTGGAGTTATGATTCTCTCAAAAACCTTCGCCAGATCTCACTCTCGTTTCAAAC 191
DB 80 AGAAGCTGGAGCTATGATTCTCTTAAAAACCTTCGTCAGATTTCTCCAGCGCTTCAGAAT 139
QY 192 CATCTCAAGCAGGTGACCTTACGCTATGCTGTGCTTTAGTGGCATCGGTGCTGGGGCT 251
DB 140 CATCTTAACCGGTTTATTGACCTTATGTGTGCTCTTGTGGGCTCTGCTTTGAGCT 199
QY 252 TACCTTCACATTCATGGAATATCGGTGGCCTCCCTCAACAATGGCTTCGATGGGAAGC 311
DB 200 TACCTCCATGTGCTGGAATATCGCGGTATTCCTACAACGATTGGATGTATTGGAAC 259
QY 312 ATGGTGTGGCTTCTCTCAGCTCTCTTATCAAGAGCAAAAAGGTGGCTCTTCTGATG 371
DB 260 ATGATTGGCTCTCTTTCATGTCTCTTATGAACACCAAAAAGGCTTCTTCTTCTTT 319
QY 372 GCAGCTGCATCTTTTGAAGCGCCTCTATTGCTCTCTGATTGAGCTGGGCATTAACCTC 431
DB 320 CGGCTGCTGTTCTTGAAGTGCTCTGTGGCCCTTGTGATCAAGTGGCAATTGATGT 379
QY 432 GATCCAAGCATTTGTTGGCGCTTTTGTAGTTGTGCTGTGTTTGGTGTGCTCTCA 491
DB 380 GACCAAGCATCTTATCACTCGGTTTGTGAATCGGATAGCGTTGTCTGTCTTCTCA 439
QY 492 GCTGCTGCCATGTGGCAAGGCGCAGGGAGTACTTGTACCTCGGGGCGCTTCTTTCATCT 551

```

Db 307 TCTCTGTGATGCGCTTCGGCTTGTTCAGGGCGCTTCATTTGGACCTCTGATGATTTG 366
Qy 420 GGCATTAACTTCGATCCAAAGCATTTGTTTGGCGCTTTTGTAGGTGTGCTGTGTTTTT 479
Db 367 GCTATTGCCATTGATCTAGCTTATTTGTAGTGCATTTTGTGGCAATCTCTTTGGCTTTT 426
Qy 480 GGTGTCTCTCAGCTGTGCGCATTTGTTGGCAAGCGCAGGAGTACTTGTACCTTCGGGGC 539
Db 427 GCTTGTCTCTCAGCTGTGCGCATTTGTTGGCAAGCGCAGGAGTACTTGTACCTTCGGTGT 486
Qy 540 CTTCCTTTCATCTGCGCTCTCCCTCTCTCTCTGTTGCACCTTTCGACCTTCCTCCATTTTGT 599
Db 487 TTGCTTTCTTCTGGCTGTGCTTCTCTCTCTCTGTTGCACCTTTCGACCTTCTCTCTCTTGG 546
Qy 600 GGTTCATGCTGTTTTCAAGTTTGAAGTTTGGCTGTTTTGGACCTTGTGCTTGGGCTAC 659
Db 547 GGTCAATTTGACCTCTTCAAGTTTGAAGTTTGGCTGTTTTGGACCTTGTGCTTGGGCTAC 606
Qy 660 ATGCTCTTTTGACACCCAAAGAAATTAATTGAGAAGGCTCCTCTGGGTGATATGATTAAGTT 719
Db 607 GTTTTGTAGACACTCAAGAAATTAATTGAGAAGGCTCCTCTGGGTGATATGATTAAGTT 666
Qy 720 AAGATGATTAAGCTTTTCAAGATTTTGGGCTGTTTTGGCTGTTTTGGCTGTTTTGGCTG 779
Db 667 AAGATGATTAAGCTTTTCAAGATTTTGGGCTGTTTTGGCTGTTTTGGCTGTTTTGGCTG 726
Qy 780 ATGTTAAAGATGATCTGAGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 826
Db 727 ATGTTGAAGATTCATTTGGGGGAATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 773

RESULT 5
US-10-219-220-232
; Sequence 232, Application US/10219220
; Publication No. US20030082724A1
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of plant development
; FILE REFERENCE: 11000.1022c1
; CURRENT APPLICATION NUMBER: US/10/219,220
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 232
; LENGTH: 1218
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-219-220-232

Query Match 39.7%; Score 411; DB 9; Length 1218;
Best Local Similarity 74.2%; Pred. No. 4.4e-118;
Matches 519; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

Qy 130 GCAACCGCTGGAGTTATGATTTCTCAAAAGCTTCGGCAGATCTCACCTCTCGTTCAAA 189
Db 157 GCAAGGGTGGAGCCAGATTTCTTCAAGATTTCTCGCAGATATCTCCGCGCTCCAA 216
Qy 190 CTCACTCAAGAGGTTACCTTACCTATGCTATGCTGCTTTAGTGGCATCGCTCGGG 249
Db 217 CTCACCTCAAGATTTATCTGCTTATGCTGCTTTATGCTGCTTTGCTGCTTCCGCGGTG 276
Qy 250 CTTACCTCTCACATTTCTGATATCGTGGCTCTCTCACAAATGCTTGCATGGAA 309
Db 277 CTTACCTGATCTGATGCTGAATCTCGGCGGCTCTCTCAAGATTTCTTGCATCGAA 336
Qy 310 GCATGTTGGCTTCTCTCAGCTCTCTCTTATCAAGAGCAAAAGGTTGCTCTTCTGA 369
Db 337 GCATTTGTTGGCTTCTCTCAGCTCTCTCTTATCAAGAGCAAAAGGTTGCTCTCTCTCA 396

Qy 370 TGGCAGCTGCACCTTTTGAAGCGCGCTCTATTGCTCTCTGATTGAGCTGGGCAATTAAC 429
Db 397 TGGCGGGCTCTCTTTTGAAGCGGTGCTATTGCTCTCTCATCGACGCGCCCAATTAAGG 456
Qy 430 TCGATCAAGCATTTGTTTGGCGCTTTTGTAGGTGTGCTGCTGTTTGTGTTGCTTCT 489
Db 457 TCGACCCGAGCATTTGTATAAGCGCAATTTGTGGGATCTGCGCTGGCCTTGGCTTGTCT 516
Qy 490 CAGCTCTGCCATTTTGGCAAGCGCAGGAGTACTTGTACCTCGGGGCGCTTCTTTCAT 549
Db 517 CGGCGCAGCCATTTTGGCTAGCGGAGGAGTACCTATATCTTTGGTGGCTTGTCTTCT 576
Qy 550 CTGCGCT 609
Db 577 CTGCGCT 636
Qy 610 CTGTTTCAAGTTTGAAGTTTGTGAGTCTTGTGCTCTTGTGCTCTCTCTCTCTCTCT 669
Db 637 CCACTTTAAGTTTGAAGTATCTTTGGCTTTTGTAGTGTTCATCGGCTATGTTGCTG 696
Qy 670 ACACCCAAAGAAATTAATTGAGAAGGCTCCTTGGGTGATATGATTAAGCATGAT 729
Db 697 ACACCTCAAGAGATAATCGAGCTAGCACACCGGCTGATATGATTAAGCATGAT 756
Qy 730 TGACCTTTTCAAGATTTTGGCGCTTGTGCTGCTTGTGCTGCTTGTGCTGCTTGT 789
Db 757 TGAACCTCTTCT 816
Qy 790 ATGCATCTGAGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 828
Db 817 ACTCTGCGAG 855

RESULT 6
US-10-167-015-31
; Sequence 31, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Uhal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (72)... (830)
US-10-167-015-31

Query Match 30.4%; Score 314.4; DB 9; Length 1026;
Best Local Similarity 65.9%; Pred. No. 7.8e-88;
Matches 456; Conservative 0; Mismatches 236; Indels 0; Gaps 0;

Qy 134 CGCTGGAGTTATGATTTCTCAAAAGCTTCGGCAGATCTCACCTCTCGTTCAAACTCA 193
Db 128 CGATGGAGCTACGATCTCAAGAACTTCGGCAGATCACCCCGCGCTCCAGACCCA 187
Qy 194 TCTCAAGCAGGTGTACCTTACGCTATGCTGCTTTTGTGCTGCTGCTGCTGCTGCT 253
Db 188 CCTCAAGCTGCTTACCTCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 247

Qy	254	CCTTCACATTCCTATGGAATATCGGTGGCCCTCTCAACAATATGGCTTGCAATGGGAAGCAT	313
Db	248	CCTGCACGTGGTCTCGAAATACATCGCGCGTACGCTGACAAATGCTCGGTTTCGGTCGCGACGAT	307
Qy	314	GGTGTGGCTTCTCTCAGCTCCTCTTATCAAGAGCAAAAAGGGTGGCTCTCTCTGATGGC	373
Db	308	CGCTTGGCTCTTCTCGGTGCCGCTACGAGGAGAGAGATATGGCTGCTGATGGC	367
Qy	374	AGTGCACATTTTGAAGCGGCTCTATTGGTCTCTGATTGAGCTGGGCATTAACATTGCA	433
Db	368	GGTGCCTCTCTCGAAGCGCTTCGGTCGACGCCCTCGTCAAGCTCGCGGTGGAAATTGA	427
Qy	434	TCCAAGCATGTGTTTGGCGCTTTTGTAGCTTGTGCTGTGGTTTGTGGTTCCTTCTCAGC	493
Db	428	CCCAAGCATCTGGTGTGACGGGGTTCGTGGGGAAGTCCATCGGTTTCGGGTCTTTCACCG	487
Qy	494	TGTCGCATGTGGTGCAGAGCGCAGGAGTACTTGTATCTTCGCGGGCTTCTTTCACTCG	553
Db	488	CGCGGCATGTGGTGCAGCGCAGGAGTACTTCTACCTGGGTGGGTGCTCTCGTCGGG	547
Qy	554	CGTCTCCCTTCTCTCTCGTGTGCACTTTTGATCCTCCATTTTGGTGGTTCCATGGCTGT	613
Db	548	GCTCTCCATCTCTCTGGCTGCAGCTAGCGGCTCCATCTTCGCGCACTCGCAACAG	607
Qy	614	TTTCAAGTTTGAGTTGTAATTTTGACTCTTGTGTGTGGCTACATCGTCTTTGACAC	673
Db	608	CTTCTATGTTGAGGTCTACTTCGGGCTGCTCATCTTCTCGGCTACGTGGTGTACGAC	667
Qy	674	CCAAGAAATTAATGAGAAGGCTCACTTGGGTGATATGGATTACGTTAAAGCATGCAATTGAC	733
Db	668	GCAGGAGATCATGAGAGGGCCACCGCGCGACATGGACCAGTCAAGCACGCCCTCAC	727
Qy	734	CCCTTTTCAAGATTTTGGCGCTGTTTTTGGCGGATCTCTGATCATCATGTTAAAGATGC	793
Db	728	CCCTTTCACAGACTTCGTGGCGGCTCCTCGTCGGCTCTCGTCTATCATGCTCAAGAACGG	787
Qy	794	ATCTGAGAAGGAGAAGAAGAAGAGGA	825
Db	788	GGCGCAAGTTCGGAGGACAAGAGAGAGA	819

RESULT. T 7

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US-10-167-015-1
; Sequence 1, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johar, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 957
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (72)...(823)
US-10-167-015-1

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134	QY	CGGTGGAGTTATGATTTCTCTCAAAAACTTCGGCAGATCTCACCTCTCTGTTCAAACTCA	193
135	QY	CGGTGGAGTTATGATTTCTCTCAAAAACTTCGGCAGATCTCACCTCTCTGTTCAAACTCA	194
136	DB	CGGAGCGGCTTCGAATTCGCTCAAGCGTCTGGGTCACTCATCTACCCGCTGTGAGTCCCA	175
137	QY	TCTCAAGCAGGTGTACCTTACGCTATGCTGTGCTTTAGTGGCATCGGCTCTCGGGCTTA	253
138	DB	CCTCAACATGTGTACTCTCACCTATGCTCCGCTGGCCTTCTTCGACCTCGCGCGTA	235
139	QY	CCTTCACATTTCTATGGAATATACGTTGGCTCTCTCAACAATAGCTTGCATGGAAGCAT	313
140	DB	CCTCACAATCTCTCTCAACGTCGGAGCGCCTCACGACCGTGGATGCGTGCCTCCAT	295
141	QY	GGTGTGACTCTCTCT-----CAGCTCTCTCTTATCAAGAGCAAAAAAGGCTGCTCTTCT	367
142	DB	GGCCTTCTCATCTCCCTGCCGCTTCAGGGGACGAGGAGAACCGCTTGGCGTGTCT	355
143	QY	GATGGCAGCTGCACCTTTTGAAGCGCCTCTATTTGGTCTCTGTATTCGAGCTGGCATTA	427
144	DB	CATGTCGCGCGCTCTTTCAAGGCGCTGCTGTCGCTCGTCGACCTTGTATTGA	415
145	QY	CTTCGATCCAAGCATTTGCTTTGGCGCTTTTGTAGTTGCTGCTGCTTTTTCGTTGCTT	487
146	DB	CTTGGATTTCAGAGATCTCTGTCATCTGCGTTCGTCGGGACCGCAGTTCCTTTTCATGCTT	475
147	QY	CTCAGCTCTCTGCCATGTTGGCAAGCGCAGGGAGTACTGTGTACCTCGGGGCGCTTCTTC	547
148	DB	CTCTGGCGCTGCCATCATCGCCAAGCGCAGGGAATACCTGTACCTCGCGGCTCTGCTTC	535
149	QY	ATCTGGCGCTCCCTCTCTCTCTGGTGCACCTTTCATCTCCATTTTTCGTTGGTTCAT	607
150	DB	ATCTGGCGCTCCCATCTCTCTCTGGCTGAGTTGCTGCTGCTTACTTTCGGCACCCAG	595
151	QY	GGCTGTTTTCAAGTTTCAGTTGTATTTTTCGACTCTTGTGTTTCTTGGGCTACATCGTCTT	667
152	DB	CGCGACCTTCATGTTTGAGCTCTACTTTTGGCCTCTCTGTTTCTCGGATATATGTTGT	655
153	QY	TGACACCCAGAAATTTTGAAGAGGCTCACTTGGGTGAATGATTAAGTAAAGCATGC	727
154	DB	TGACACCCAGAGATCATTCAGAGGGCGCACCGTGGGACATGCACTACATCAAGCACGC	715
155	QY	ATTGACCTTTTTCACAGATTTTGGCGCTGTTTTTCTGCGGATTCGTATCATCTGTATAA	787
156	DB	GCTGACTCTTTCACCGACTTTTCTGGGTTCTTGTTCGAATCTTGTCTCATCATGATA	775
157	QY	GAATGCATCTTCAGAAGGAAGAGAAGAAAGAGAGAGAA	829
158	DB	GAATGCACAGAGAGAAATCCCAACAGCAGAGAAGAAAGAGAGAA	817

RESULT 8

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RESUL 8
US-10-167-015-33
; Sequence 33, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 1138
; TYPE: DNA
; ORGANISM: Zea mays

```

```
;
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (136)...(912)
US-10-167-015-33

Query Match      30.0%; Score 310.4; DB 9; Length 1138;
Best Local Similarity 64.8%; Pred. No. 1.5e-86;
Matches 477; Conservative 0; Mismatches 256; Indels 3; Gaps 1;

Qy 96 TTCAATGTTTCTTCGACTCGCAATCTGCCTCTCGCAACCGCTGGAGTTATGATTCTCTC 155
Db 166 TCCTCCACGTCGTGCGCGCGTACGCGCGCGCGGAGGCTGGGCTACGACTCGATG 225

Qy 156 AAAAATTCGCGAGATCTACCTCTCTGTTCAAATCTCATCTCAAGCAGGTGTACTTACG 215
Db 226 AAGAACTTTCGCGAGATCAGCCCGCGCTCCAGACCCACCTCAAGCTCGTTTACCTCACC 285

Qy 216 CTATGCTGTCTTTAGTGGCATCGGCTGTGGGGCTTACCTTCACATTCATGGAATATC 275
Db 286 CTATGCTGTGGCTGTGCGCTGTGCGGGTGGGCGGTACCTGCACGTCGTGGAACATC 345

Qy 276 GGTGGCTCTCTCAACAATGGCTTCATGGAAGAGTGTGTGCTTCTCTCAGCTCCT 335
Db 346 GCGGGATGTGACCATGTCTCGGCTCGGTCGCGCAGCATGCGCTCTCTCTCGGTGCC 405

Qy 336 CCTTATCAAGAGCAAAAAGGGTGGCTCTTCTGATGGCAGCTGCACCTTTTGAAGCGCC 395
Db 406 GTCTACGAGAGAGAGAGGTACTGGCTGTGATGGCGGCTGCCCTCTCTGGAAGGGCG 465

Qy 396 TCTATTGGTCTCTGATGAGCTGGGCAATACTTCGATCCAAAGCATTTGTTGGCGCT 455
Db 466 TCGTTGGACCCCTCATCAAGCTCGCGCTGGAATTGACCCAGCATCTCTGTGACAGCG 525

Qy 456 TTTGTAGTTGTCTGTGGTGTGTTTGGTGTCTCTCATGGCAGCTGCACCTTTTGAAGCGCC 515
Db 526 TCTGTGGGACTGCCATGCGTTTCGGTGTGCTTCTCTGCGCGCCATGGTGGCCAGCGC 585

Qy 516 AGGAGTACTTGTACCTCGGGGCTTCTTTTTCATCTGGGCTCTCTCTCTCTCTCTCTCT 575
Db 586 AGGAGTACTTACCTTACCTGGGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 645

Qy 576 CACTTTCATCTCCATTTTGG---TGGTTCATGGCTGTGTTTCAAGTTTGAAGTTGAT 632
Db 646 CAGTTCGCGCTCCATCTTCGCGCCACCAATCCATAGCAGCTTCATGTTGAGGTCTAC 705

Qy 633 TTTGAGCTCTTGTGTTGTGGCTACATGCTTTTGAACCCAAAGAAATTTAGAGAG 692
Db 706 TTTGGGCTGTCTATCTCTCTGGCTACATGCTGTGTACACACGAGAGGTCTATCGAGAG 765

Qy 693 GCTCATTGGGTGATGATTACGTTAGCATGCTTACCCCTTTTACAGATTTTGGC 752
Db 766 GCGCACACGCGACATGAGTACATCAAGCAGCCCTCACCTCTTCCACGACTTCGTG 825

Qy 753 GCTGTTTTTGTGGGATTTCTGATCATCATGTTTAAAGATTCATCTGAGAGAGAGAG 812
Db 826 GCTGTCTTGTTCGCAATCTTGTTCATCATGCTCAAGACGCGGCTGACAAAGTCGAGGAC 885

Qy 813 AAGAGAGAGAGAGAA 828
Db 886 AAGAGAGAGAGAGGA 901

;
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1139
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (136)...(993)
US-10-167-015-5

Query Match      30.0%; Score 310.4; DB 9; Length 1139;
Best Local Similarity 64.8%; Pred. No. 1.5e-86;
Matches 477; Conservative 0; Mismatches 256; Indels 3; Gaps 1;

Qy 96 TTCAATGTTTCTTCGACTCGCAATCTGCCTCTCGCAACCGCTGGAGTTATGATTCTCTC 155
Db 166 TCCTCCACGTCGTGCGCGCGTACGCGCGCGCGGAGGCTGGGCTACGACTCGATG 225

Qy 156 AAAAATTCGCGAGATCTACCTCTCTGTTCAAATCTCATCTCAAGCAGGTGTACTTACG 215
Db 226 AAGAACTTTCGCGAGATCAGCCCGCGCTCCAGACCCACCTCAAGCTCGTTTACCTCACC 285

Qy 216 CTATGCTGTCTTTAGTGGCATCGGCTGTGGGGCTTACCTTCACATTCATGGAATATC 275
Db 286 CTATGCTGTGGCTGTGCGCTGTGCGGGTGGGCGGTACCTGCACGTCGTGGAACATC 345

Qy 276 GGTGGCTCTCTCAACAATGGCTTCATGGAAGAGTGTGTGCTTCTCTCAGCTCCT 335
Db 346 GCGGGATGTGACCATGTCTCGGCTCGGTCGCGCAGCATGCGCTCTCTCTCGGTGCC 405

Qy 336 CCTTATCAAGAGCAAAAAGGGTGGCTCTTCTGATGGCAGCTGCACCTTTTGAAGCGCC 395
Db 406 GTCTACGAGAGAGAGAGGTACTGGCTGTGATGGCGGCTGCCCTCTCTGGAAGGGCG 465

Qy 396 TCTATTGGTCTCTGATGAGCTGGGCAATACTTCGATCCAAAGCATTTGTTGGCGCT 455
Db 466 TCGTTGGACCCCTCATCAAGCTCGCGCTGGAATTGACCCAGCATCTCTGTGACAGCG 525

Qy 456 TTTGTAGTTGTGCTGTGGTGTGTTTGGTGTCTCTCATGGCAGCTGCACCTTTTGAAGCGCC 515
Db 526 TTTGTGGGACTGCAATTTGG---TGGTTCATGGCTGTGTTTCAAGTTTGAAGTTGAT 632

Qy 576 CACTTTCATCTCCATTTTGG---TGGTTCATGGCTGTGTTTCAAGTTTGAAGTTGAT 632
Db 646 CAGTTCGCGCTCCATCTTCGCGCCACCAATCCATAGCAGCTTCATGTTGAGGTCTAC 705

Qy 633 TTTGAGCTCTTGTGTTGTGGCTACATGCTTTTGAACCCAAAGAAATTTAGAGAG 692
Db 706 TTTGGGCTGTCTATCTCTCTGGCTACATGCTGTGTACACACGAGAGGTCTATCGAGAG 765

Qy 693 GCTCATTGGGTGATGATTACGTTAGCATGCTTACCCCTTTTACAGATTTTGGC 752
Db 766 GCGCACACGCGACATGAGTACATCAAGCAGCCCTCACCTCTTCCACGACTTCGTG 825

Qy 753 GCTGTTTTTGTGGGATTTCTGATCATCATGTTTAAAGATTCATCTGAGAGAGAGAG 812
Db 826 GCTGTCTTGTTCGCAATCTTGTTCATCATGCTCAAGACGCGGCTGACAAAGTCGAGGAC 885

Qy 813 AAGAGAGAGAGAGAA 828
Db 886 AAGAGAGAGAGAGGA 901

;
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; Sequence 5, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A.
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
```

```

RESULT 10
US-10-167-015-3
; Sequence 3, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; TITLE OF INVENTION: Theresof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (72)....(830)
US-10-167-015-3

Query Match      29.5%; Score 305; DB 9; Length 1026;
Best Local Similarity 65.9%; Pred. No. 6.9e-85;
Matches 457; Conservative 0; Mismatches 235; Indels 1; Gaps 1;

QY 134 CCGTGAGTATGATTTCTCTCAAAACCTTCGCCAGATCTCACCTCTCGTTCRAACTCA 193
DB 128 CGATGAGAGTACGATCGCTCAAGAACTTCGCCAGATCACCCCGCGCTCAGACCCA 187
QY 194 TCTCAAGCAGGTGATCTACCTATGCTGTGCTTTAGTGGCATCGGCTGTGGGGCTTA 253
DB 188 CCTCAAGCTCGTCTACCTACCTACCTGTGCGCGGCTGGCTCGTGGCGGTGGGCTTA 247
QY 254 CCTTCACATCTATGAATATCGGTGGCTCTCTCAACAACATGGCTTGATGGGAAGCAT 313
DB 248 CTTGCAGCTGGTCTGGAAATATCGCGGTACCTGTGACATGCTCGGTGGCTCGGAGCAT 307
QY 314 GGTGTGCTCTTCTCAGCTCTCTCTATCAAGAGCAAAAGAGGTGGCTCTTCTGATGCG 373
DB 308 CGCTGCTCTTCTCGTGGCTCTACGAGGAGAGAGAGGTATGGCTCTGATGCG 367
QY 374 AGTGCACATTTTGAAGCGGCTCTATTGCTCTCTGATTGAGCTGGGCATTAACCTCGA 433
DB 368 GGTGCGCTCTCTGGAAGGCTCTCGGTGGACCCCTCGTCAAGCTCGCGTGGAAATTGA 427
QY 434 TCCAAGCATGTGTTTGGCGCTTTTGTAGTGTGCTGTGCTGTGTTTGTGTTTGTCTCAGC 493
DB 428 CCCAAGCATCTGTGTGACGGGTCTGTGGGACTGCCATCGGCTTCGCGTCTCACCGG 487
QY 494 TGTGCGCATGTGGCAAGGCGCAGGAGTACTTGTACTCTCGGGGCTCTTCTCTGCTGG 553
DB 488 CGCGGCGCATGTGGCCAGGCGCAGGAGTACCTCTACCTGGGTGGGCTCTCTCGTGGG 547
QY 554 CGTCTCCCTCTCTCTGTGTGCACTTTGATCTCTCATTTTGTGTGTTCATGGCTGT 613
DB 548 GCTCTCCATCTGTCTGTGTGAGCTAGCTAGCGGCTCCATCTTCGGCCACTCCGCAACG 607
QY 614 TTTCAAGTTTGTGTTTATTTGACATCTTGTGTTTGTGGGTACATCGCTTTTGACAC 673
DB 608 CTTTATGTTGAGGTCTACTTCGGGCTGTCTCATCTTCCTGGGTAGTGTGTGACAC 667
QY 674 CCAAGAAATTTTCAAGAGGCTCACTTGGGTGATGATGATTTAGTTAAGCATGCAATTGAC 733
DB 668 CGAGGATCATCGAAGGGCGACCGCGGACATGGACCATGTCAGCACGCCCTCAC 727

QY 734 CTTTTTCACAGATTTTGGCGCTGTTTGTGGGATTTCTGATCATCATG-TTAAAGATG 792
DB 728 CTTCTTTCACAGATTTCTGTGGCGCTTCGTGCGGCTCTCTGTCATGCTCAAAGAAGC 787
QY 793 CATCTGAGAAGGAGAGAGAGAGAGAGAGAGGA 825
DB 788 GGGCCGACAACTCGGAGGACAAAGAGAGAGA 820

RESULT 11
US-10-219-220-231
; Sequence 231, Application US/10219220
; Publication No. US20030082724A1
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Amette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of plant development
; FILE REFERENCE: 11000.1022c1
; CURRENT APPLICATION NUMBER: US/10/219,220
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 231
; LENGTH: 1102
; TYPE: DNA
; ORGANISM: Pinus radiata
US-10-219-220-231

Query Match      23.8%; Score 245.6; DB 9; Length 1102;
Best Local Similarity 60.6%; Pred. No. 3.1e-66;
Matches 423; Conservative 0; Mismatches 269; Indels 6; Gaps 1;

QY 137 CTGGAGTATGATTTCTCAAAACCTTCGCCAGATCTCACCTCTCGTTCAAACTCATCT 196
DB 154 CTGGATTAACAATGTTATGAGACATGAAAAGATGAGCCCTGCGGTGAGATCATCT 213
QY 197 CAAGCAGGTGTACCTTACGCTATGCTGTCTTTAGTGCAATCGGCTGTGGGGCTTACCT 256
DB 214 GAAAGGGTTTATTGTGCTTAGCTGTGCTGCTGTAACAGCAGCATCGGTGTTTATT 273
QY 257 TCACATCTCATGATATCGGTGGCTCTCTCACACATGCTTGCATGGGAAGCATGGT 316
DB 274 GCATCTCTGTGTAATATTGGAGGCTCTCTCACGGGCTCTCTGATGTTCTGTAAT 333
QY 317 GTGGCTTCTCTCAGCTCTCTCTT-----ATCAAGAGCAAAAGAGGTGGCTCTTCTGAT 370
DB 334 CGGGCTTTATCGTCCCTACTTCTCGAACAAATGAGGTAAGAGAGCTGGCTGCTCCT 393
QY 371 GGCAGTGCACATTTTGAAGGCGCTCTATTGGTCTCTGATTGAGCTGGGCATTAACCT 430
DB 394 GGCAGTGTGCTGTTCAAGGGAGCTACTTGGGACCGCTCATCGACGCGTCAATATAT 453
QY 431 CGATCCAAGCATGTGTTTGGCGCTTTTGTAGTGTGCTGTGTTTGTGTTTGTGTTCTC 490
DB 454 TGACTCAATATACCTGGTGTGCTGTTTGGGACCTTTTGGCTTCGCTTCTTTC 513
QY 491 AGTGTGCTGCATGTTGGCAAGCGCAGGAGTACTTGTACTCTCGGGGCTCTTCTTCTC 550
DB 514 GGCAGCAGCAATACACAGCCAGGAGACGGGAATACCTATTTTGGGAGGATTAATGGGCTC 573
QY 551 TGGCGTCTCCCTCTCTCTGTTGCTCTTTCATCTCTCCATTTTGGTGTGTTCCATGGC 610
DB 574 GGAATCAGCATATTAATGATGTGCTGCACTAGCATCTCGATTTTGGTGTCTTCTGCGC 633
QY 611 TGTTTCAAGTTTGTGTTTATTTGGACTCTTGTGTTTGTGGGTACATCGTCTTTGA 670
DB 634 GATTTACATTTGATCTACTTCCGTCTGCTAGTTTTCCTTGGGTATATATATTGA 693
QY 671 CACCCAGAAATTTATTGAGAAGGCTCACTTGGGTGATATGATTAAGTAAAGCATGCAAT 730
```

Db 694 CACACAGATGATCATCGAGAAAGCGACCAATGAGACTATGATTAATAAAATCACT 753
Qy 731 GACCTTTTACAGATTTGGCGCTGTTTTTGTGGGATTTCTGATCATCATGTTAAAGAA 790
Db 754 GGACCTTTTACATGCTGTTGCTGATTTTGTGCTGATGATGATGATGATGATGAT 813
Qy 791 TGCATCTGAG 828
Db 814 TGCAGACAGTAATCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 851

RESULT 12
US-10-219-220-43
; Sequence 43, Application US/10219220
; Publication No. US2003008274A1
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; FILE OF INVENTION: death and their use in the modification of plant development
; FILE REFERENCE: 1100.1022c1
; CURRENT APPLICATION NUMBER: US/10/219,220
; PRIOR FILING DATE: 2002-08-14
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 884
; TYPE: DNA
; ORGANISM: Pinus radiata
US-10-219-220-43

Query Match 21.4%; Score 221.2; DB 9; Length 884;
Best Local Similarity 60.6%; Pred. No. 1.2e-58;
Matches 383; Conservative 0; Mismatches 243; Indels 6; Gaps 1;

Qy 203 GGTGTACCTTACGCTATGCTGCTTTAGTGGGATCGGCTGCTGGGCTTACCTTACAT 262
Db 4 GGTTTATTTGTCGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 63
Qy 263 TCTATGGAATATCGGTGCTGCTTCTCACAAATGCTTGTATGGAGAGATGCTGCTGCT 322
Db 64 TCTGTTGATATGAGGGCTTCTCACGGGCTGCTTGTGCTGCTGCTGCTGCTGCTGCT 123
Qy 323 TCTCTAGCT 376
Db 124 CTATCCGCTCCCTACT 183
Qy 377 TGCACCTTTTGAAGGCGCTCTATTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 436
Db 184 TCTGCTGCTTCAAGGAGTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 243
Qy 437 AAGCATTTGTTTGGCGCTTTTGTAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 496
Db 244 CAGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 303
Qy 497 TGCATTTTGGCAAGCGCAGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 556
Db 304 AGCAATCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 363
Qy 557 CTCCCT 616
Db 364 CAGCATATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 423
Qy 617 CAGTTTGTAGTTGATTTTGGACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 676
Db 424 CACATTTGAGATCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 483
Qy 677 AGAAATTTTGAAGGCT 736
Db 484 GATGATCATCGAG 543

Qy 737 TTTCACAGATTTTGGCGCTGTTTTTGTGGGATTTCTGATCATCATGTTAAGATGCTC 796
Db 544 CTTCAATGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 603
Qy 797 TGAGAAGGAG 828
Db 604 CAGTAATCCAGGAG 635

RESULT 13
US-10-219-220-44
; Sequence 44, Application US/10219220
; Publication No. US2003008274A1
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; FILE OF INVENTION: death and their use in the modification of plant development
; FILE REFERENCE: 1100.1022c1
; CURRENT APPLICATION NUMBER: US/10/219,220
; PRIOR FILING DATE: 2002-08-14
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 527
; TYPE: DNA
; ORGANISM: Pinus radiata
US-10-219-220-44

Query Match 21.2%; Score 219.2; DB 9; Length 527;
Best Local Similarity 74.5%; Pred. No. 3.6e-58;
Matches 289; Conservative 0; Mismatches 98; Indels 1; Gaps 1;

Qy 130 GCAACCCCTGAGTTATGATTTCTCTCAAAAATTTCCGCCAGATCTCACCTCTCGTTCAA 189
Db 141 GCAAGGGGTGAGCCAGATTCCTCTCAAGAACTTCGCCAGATATCTCCGCCGCTCCAAT 200
Qy 190 CTATCTCAAGAGGTGTACCTTACCTATGCTGCTTGTAGTGCATCGGCTGCTGGG 249
Db 201 CTCACTCAAGAAATGTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 260
Qy 250 CTTACCTTCACTTATGAAATATCGGTGGCTCTCTCAACAATGCTTGCATGGGAA 309
Db 261 CTTACCTTCACTTATGAAATATCGGTGGCTCTCTCAACAATGCTTGCATGGGAA 320
Qy 310 GCATGCTGCT 369
Db 321 GCATGCTGCT 380
Qy 370 TGGCAGCTGCACTTTTGAAGGCGCTCTATTTGCTCTCTCTCTCTCTCTCTCTCTCTCT 429
Db 381 TGGGCGGCT 440
Qy 430 TCGATCAAGAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 489
Db 441 TCGACCCGAGCATTTGATTAAGGCGCATTTGTGGGATCTCGCTGGCTTCTGCTTCT 500
Qy 490 CAGCTGCTGCCATTTTGGCAAGGCGAG 517
Db 501 CGGCGCAG-CATGTTGGCTAGCGGAG 527

RESULT 14
US-10-167-015-7
; Sequence 7, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro

```

; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 740
; TYPE: DNA
; ORGANISM: zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)...(489)
US-10-167-015-7

Query Match      17.3%; Score 178.8; DB 9; Length 740;
Best Local Similarity 64.0%; Pred No. 2.1e-45;
Matches 270; Conservative 0; Mismatches 152; Indels 0; Gaps 0;

QY 404 TCCTCTGATGAGCTGGGCAATTAACCTGATCCAGCATGTGTGTCGCTTTGAGG 463
Db 57 TGCTTAGATGACGAATGGCTGTTTTTTTCCCTCAGCATCTCTGTGACGGGTTTCGTGG 116
QY 464 TTGTGCTGTGTTTTTTGTTGCTTCTCAGCTGCTGCCATGTTGGCAAGCGCAGGAGTA 523
Db 117 GACTGCCATCGCTTCGCTGCTTTACCGCGCGGCCCATGTGGCCAGCGCAGGAGTA 176
QY 524 CTTGTACCTCGGGGGCTTCTTTTCATCTGGCGTCTCCCTTCTCTCTGTTGCCACTTGC 583
Db 177 CCTCTACCTGGGTGGCTGCTCTCGTGGGGCTCTCCATCTCTGCTCTGCTGACGTAGC 236
QY 584 ATCTCCATTTTGGTGGTTCATGCTGTTTCAAGTTGAGTTGATTTGGACTCTT 643
Db 237 CGGCTCCATCTTCGGGCACCTCGCAACCAAGCTTCATGTTGAGGTTCTACTTCGGGCTCT 296
QY 644 GGTGTTTGTGGGCTACATCGTCTTTGACACCCCAAGAAATTTAGAAAGGCTCACTTGGG 703
Db 297 CATCTTCCTGGGCTACGTGTGTACGACACGCGAGGAGATCATCGAGAGGGCGCACCGGG 356
QY 704 TGATATGATGATTAGTTAAGCATGCTATGCCCTTTTCACAGATTTTGGCGTGTGTTGT 763
Db 357 CGACATGGACACGCTCAAGCACCCCTCACCCTCTTTCACAGACTTCTGTGGCGGCTCCTGT 416
QY 764 GCGGATTCATCATCATGTTAAAGATGATCTGAGAAGGAAGAGAGAGAGAGAG 823
Db 417 CCGGCTCTCTCATCATGCTCAGAACGGGGCCGACAGTCTGGAGGACAGAGAGAA 476
QY 824 GA 825
Db 477 GA 478
```

```

RESULT 15
US-10-167-015-22
; Sequence 22, Application US/10167015
; Publication NO. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
```

```

; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 308
; TYPE: DNA
; ORGANISM: glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(308)
; OTHER INFORMATION: n = A,T,C or G
US-10-167-015-22

Query Match      17.2%; Score 177.8; DB 9; Length 308;
Best Local Similarity 75.6%; Pred. No. 2.4e-45;
Matches 232; Conservative 0; Mismatches 74; Indels 1; Gaps 1;

QY 453 GCTTTTGTAGGTTGTGCTGTGTTTTTTGGTTGCTTCTCAGCTGCTGCCATGTGGCAAGG 512
Db 2 GCATTTGTGGGAACATCCTTGGCCTTTTGCATGCTTCTCAGGACAGCTTTGGTTGCTAGG 61
QY 513 CGCAGGGAGTACTTGTACTCGGGGGCTTCTTTTCATCTGGCGTCTCCCTTCTCTTCTGG 572
Db 62 CGTAGGGAGTACTTGTACTTGTGGTGGCTTGTCTTCTGTGATTGTCATCTCTCTGG 121
QY 573 TTGCACCTTGTGATCCTCCATTTTGTGGTGGTTCATGGCTGTTTTCAAGTTTGTGTTGAT 632
Db 122 TTGCACCTTGTCTTCTCCATCTTTTGGAGTTCAACAGCTCTCTTTAAAGTTTGTGTTGAT 181
QY 633 TTTGGACTCTTGGTGTGTTTGTGGGCTACATCGTCTTTGACACCCC-AAGAAATTTAGAGAA 691
Db 182 TTTGGGCTTTTGGTGTGTTTGTAGTTTACATTTAGTACACCCCAAGAAATAGTTAGAN 241
QY 692 GGCTCACCTTGGGTGATATGGATTACGTTAAGCATGCAATGACCCCTTTTTCAGATTTTGG 751
Db 242 GGCACACTTGGGCGATCTGGACTATGTAAGCATGCCCTTGACCTTGTTTACCGATTGSGN 301
QY 752 CGCTGTT 758
Db 302 TGCATTT 308
```

Search completed: May 25, 2003, 12:19:38
Job time : 170 secs

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 25, 2003, 09:52:48 ; Search time 1487 Seconds

(without alignments)

11261.690 Million cell updates/sec

Title: US-09-955-526-3

Perfect score: 1034

Sequence: 1 ggcgaacataacattgtct.....ataaggaagttccttgta 1034

Scoring table: IDENTITY NUC

Gapop 10.0 , Capext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hic:*

9: gb_est1:*

10: gb_est2:*

11: gb_hic:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_man:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	717	69.3	750	12	BG124317
2	647.4	62.6	671	13	BI933489
3	643	62.2	643	10	AW096641
4	634	61.3	645	10	AW219279
5	621.8	60.1	647	12	BG127849
6	596	57.6	596	9	AI779122

7	591	57.2	592	12	BG134507
8	534.2	51.7	578	14	BQ115430
9	498.4	48.2	540	12	BF054243
10	468.8	45.3	476	13	BI935239
11	454.4	43.9	464	9	AI895377
12	449.2	43.4	617	14	BQ115431
13	437.8	42.3	456	9	AI776541
14	423	40.9	448	10	AW399750
15	422	40.8	488	12	BE918556
16	417.6	40.4	831	12	EG839316
17	416.8	40.3	424	10	AW912843
18	416.4	40.3	464	10	AW617419
19	412	39.8	428	10	AW399749
20	405	39.2	732	14	BQ023368
21	384.2	37.2	713	14	BQ91270
22	379.4	36.7	694	12	BQ646982
23	378.8	36.6	723	14	BQ856331
24	376.4	36.4	703	14	BQ863266
25	374.8	36.2	726	12	BQ648712
26	364.4	35.2	740	14	BQ255427
27	356.6	34.5	647	10	BE577220
28	350.8	33.9	847	14	BQ792694
29	348.2	33.7	681	12	BF635314
30	343.8	33.2	776	12	BQ648573
31	338.8	32.8	752	12	BQ647209
32	337.8	32.7	643	14	BQ401834
33	337.8	32.7	811	14	BQ153367
34	335.4	32.4	620	9	AI730983
35	335	32.4	621	9	AI726851
36	334.4	32.3	619	9	AI727198
37	331.4	32.1	525	9	AJ412594
38	324.6	31.4	595	9	AI166999
39	321.4	31.1	548	12	BF423787
40	320.4	31.0	391	9	AI780552
41	312.4	30.2	621	9	AI731928
42	312	30.2	978	11	AY107681
43	310.6	30.0	665	14	BQ246217
44	309.6	29.9	761	14	BQ165368
45	307.8	29.8	551	10	AW323256

ALIGNMENTS

RESULT 1
BG124317
LOCUS
DEFINITION
EST469963 tomato shoot/meristem Lycopersicon esculentum cDNA clone
ctof4l8 5' sequence, mRNA sequence.
ACCESSION
BG124317.1 GI:12624505
VERSION
BG124317.1
KEYWORDS
EST.
SOURCE
tomato.
ORGANISM
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.

REFERENCE
AUTHORS
Hansen, C., Roming, C. and Tanksley, S.
TITLE
Generation of ESTs from tomato shoot/meristem tissue
JOURNAL
Unpublished (2001)
COMMENT
Contact: CUGI

1 (bases 1 to 750)
van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Utterback, T.,
Hansen, C., Roming, C. and Tanksley, S.
Generation of ESTs from tomato shoot/meristem tissue
Unpublished (2001)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>.

FEATURES
source
1..750
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"

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/clones="CTOF418"
/clone_lib="tomato shoot/meristem"
/tissue_type="shoot/meristem"
/dev_stage="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
/notes="vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Small expanding leaves from the growing tip were
taken from greenhouse plants (4-6wks old TA496). Tissue
was immediately frozen in liquid nitrogen."
BASE COUNT      158 a 174 c 176 g 242 t
ORIGIN
Query Match      69.3%; Score 717; DB 12; Length 750;
Best Local Similarity 98.9%; Pred. No. 4.1e-173;
Matches 733; Conservative 0; Mismatches 5; Indels 3; Gaps 1;
QY 2 AGCAACATCAATGCTAGCTTACGATTAATATCTCTTCTCATTTAGTTCCAAAAA 61
DB 10 AGCAACATCAATGCTAGCTTACGATTAATATCTCTTCTCATTTAGTTCCAAAAA 69
QY 62 CTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 121
DB 70 CTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 129
QY 122 TGCCTCTCGAACCGCTGGAGTATGATTTCTCAAAATTCGCCAGATCTCACCTCT 181
DB 130 TGCCTCTCGAACCGCTGGAGTATGATTTCTCAAAATTCGCCAGATCTCACCTCT 189
QY 182 CGTTCAATCTCTCAAGCAGGTGACCTTACGATAGCTATGCTGCTTTAGTGGATCGGC 241
DB 190 CGTTCAATCTCTCAAGCAGGTGACCTTACGATAGCTATGCTGCTTTAGTGGATCGGC 249
QY 242 TGCCTGGGCTTACCTTCAATCTATGAGATATCGTGCGCTCTCTCAAAATTCGGCTTG 301
DB 250 TGCCTGGGCTTACCTTCAATCTATGAGATATCGTGCGCTCTCTCAAAATTCGGCTTG 309
QY 302 CATGGAAGAGAGTGTGTGCTCTCAGCTCTCTCTCTATCAG---AGCAAAAAGGT 358
DB 310 CATGGAAGAGAGTGTGTGCTCTCAGCTCTCTCTCTATCAGAGAGAGCAAAAAGGT 369
QY 359 GGCTCTTCTGATGGAGCTGCACTTTTCAAGCGCGCTCTATTTGCTCTGATTTAGCT 418
DB 370 GGCTCTTCTGATGGAGCTGCACTTTTGAAGCGCGCTCTATTTGCTCTGATTTAGCT 429
QY 419 GGCATTAATCTCGATCCAAGATTTGTTTGGCGCTTTTGTAGTGTGCTGTGTTTT 478
DB 430 GGCATTAATCTCGATCCAAGATTTGTTTGGCGCTTTTGTAGTGTGCTGTGTTTT 489
QY 479 TGGTGTCTTCTAGCTGCTGCCATGTTGCCAAGGCGCAGGAGTACTTTGTACCTCGGGG 538
DB 490 TGGTGTCTTCTAGCTGCTGCCATGTTGCCAAGGCGCAGGAGTACTTTGTACCTCGGGG 549
QY 539 CCTTCTTTTCTAGCTGCTGCCATGTTGCCAAGGCGCAGGAGTACTTTGTACCTCGGGG 598
DB 550 CCTTCTTTTCTAGCTGCTGCCATGTTGCCAAGGCGCAGGAGTACTTTGTACCTCGGGG 609
QY 599 TGGTTCATGCTGCTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTT 658
DB 610 TGGTTCATGCTGCTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTT 669
QY 659 CATCGCTTTTGACACCCAGAGAAATTTAGAGAGGCTCACTTTGGGTGATATGATAGT 718
DB 670 CATCGCTTTTGACACCCAGAGAAATTTAGAGAGGCTCACTTTGGGTGATATGATAGT 729
QY 719 TAAGCATGATTTGACCTTTT 739
DB 730 TAAGCATGATTTGACCTTTT 750
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RESULT 2
Bi933489 671 bp mRNA linear EST 18-OCT-2001
LOCUS Bi933489
DEFINITION EST553378 tomato flower, anthesis Lycopersicon esculentum cDNA

```
clone cTOD16N14 5' end, mRNA sequence.
Bi933489
BI933489.1 GI:16247961
EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridaceae; eusterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 671)
Location/Qualifiers
  1. 671
    /organism="Lycopersicon esculentum"
    /cultivar="TA496"
    /db_xref="taxon:4081"
    /clone="cTOD16N14"
    /clone_lib="tomato flower, anthesis"
    /tissue_type="flower"
    /dev_stage="anthesis"
    /notes="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Cornell University; sequencing: The
Institute for Genomic Research; Flower buds and flowers
were taken from greenhouse plants (4-8 wks old, TA496).
They were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
BASE COUNT      134 a 161 c 157 g 219 t
ORIGIN
Query Match      62.6%; Score 647.4; DB 13; Length 671;
Best Local Similarity 99.6%; Pred. No. 2.9e-155;
Matches 570; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
QY 12 ACATTGTCTACGTTCAAGATTAATATCTTTGCTCAATTTCAATTTCAATTTCAATTT 71
DB 1 ACATTGTCTACGTTCAAGATTAATATCTTTGCTCAATTTCAATTTCAATTTCAATTT 60
QY 72 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 131
DB 61 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 132 AACCGTGGAGTATGATTTCTCAAAAATTCGCCAGATCTCACTCTCGTTCAAAT 191
DB 121 AACCGTGGAGTATGATTTCTCAAAAATTCGCCAGATCTCACTCTCGTTCAAAT 180
QY 192 CATCTCAAGCAGGTGCTACCTTACGCTATGCTGTCTTTAGTGGCATCGGCTGTGGGCT 251
DB 181 CATCTCAAGCAGGTGCTACCTTACGCTATGCTGTCTTTAGTGGCATCGGCTGTGGGCT 240
QY 252 TACCTTCAATTTTGAATATCGTGGCTCTCTCAACAATTCGCTTCGATGGGAGC 311
DB 241 TACCTTCAATTTTGAATATCGTGGCTCTCTCAACAATTCGCTTCGATGGGAGC 300
QY 312 ATGGTGTGGCTTCTCTCAGCTCTCTCTTATCAAGAGCAAAAAGGGTGGCTCTTCTCTGATG 371
DB 301 ATGGTGTGGCTTCTCTCAGCTCTCTCTTATCAAGAGCAAAAAGGGTGGCTCTTCTCTGATG 360
QY 372 GCAGCTGCACTTTTGAAGGCGCTCTATTTGGTCTCTGATTTAGCTGGGCAATTAATTC 431
DB 361 GCAGCTGCACTTTTGAAGGCGCTCTATTTGGTCTCTGATTTAGCTGGGCAATTAATTC 420
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QY 432 GATCCAGCATTTGTTGGCGCTTTTGTAGTTGTGCTGTTTGGTGGCTTCTCA 491
DB 421 GATCCAGCATTTGTTGGCGCTTTTGTAGTTGTGCTGTTTGGTGGCTTCTCA 480
QY 492 GCTGCTGCCATGTGGCAAGCGCAGGAGTACTTGTACTCGGGGCGCTTTCATCT 551
DB 481 GCTGCTGCCATGTGGCAAGCGCAGGAGTACTTGTACTCGGGGCGCTTTCATCT 540
QY 552 GGGCTCTCCCTTCTCTTCGTTGTCATTTGTCATCTCCATTTTGGTGGCTTCCATGGCT 611
DB 541 GGGCTCTCCCTTCTCTTCGTTGTCATTTGTCATCTCCATTTTGGTGGCTTCCATGGCT 599
QY 612 GTTTTCAAGTTGAGTTGATTTTGAATCTTGGCTTGTGCTGAGTACATCTCTTTGAC 671
DB 600 GTTTTCAAG-TTGAGTTGATTTTGGACTCTTGGTGGTGTGGGCTACATCTCTTTGAC 658
QY 672 ACCCAAGAAATTA 684
DB 659 ACCCAAGAAATTA 671

RESULT 3
AW096641
LOCUS EST29821 tomato mixed elicitor, BTI Lycopersicon esculentum cDNA
DEFINITION
ACCESSION AW096641 643 bp mRNA linear EST 18-MAY-2001
VERSION clone c1ET39M7, mRNA sequence.
KEYWORDS
SOURCE EST.
ORGANISM
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE
1 (bases 1 to 643)
D'Ascenzo, M., He, X., Lyman, J., Holt, I.E., Liang, F., Upton, J.,
Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W.,
Fraser, C.M., Venter, J.C., Martin, G.B., Tanksley, S.D. and Giovannoni
J.
Generation of ESTs from tomato leaf tissue
Unpublished (1999)
CONTACT: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES
source
Location/Qualifiers
1..643
/organism="Lycopersicon esculentum"
/cultivar="Rio Grande PtoR"
/db_xref="taxon:4081"
/clone="c1ET39M7"
/clone_lib="tomato mixed elicitor, BTI"
/tissue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="X11-Blue MRF"
/note="vector: pBlueScript SK(-); Site 1: EcoRI; Site 2:
XhoI; c1ET - inoculated with a variety of disease response
elicitors. Plants exposed to 2,6 dichloroisonicotinic
acid, BTH, jasmonic acid, ethylene, fenthion, BIX,
okadaic acid, or systemin prior to tissue harvest. EcoRI
site was destroyed during cloning."
BASE COUNT 129 a 155 c 150 g 209 t
ORIGIN
Query Match 62.2%; Score 643; DB 10; Length 643;
Best Local Similarity 100.0%; Pred. No. 3.8e-154;
Matches 643; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GCAACATACATTTCTACGTTTCAGATAAATATCCTTGTCTCATTTTCAGTTCCAAAAC 62

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DB 1 GCAACATACATTTCTACGTTTCAGATAAATATCCTTGTCTCATTTTCAGTTCCAAAAC 60
QY 63 TCGAAGAAGAAGAAGAACAATGGAAGTTTCACATCGTTTCTTCGACTCGCAATCT 122
DB 61 TCGAAGAAGAAGAAGAACAATGGAAGTTTCACATCGTTTCTTCGACTCGCAATCT 120
QY 123 GCTCTCGCAACCGCTGGAGTTATGATTTCTCTCAAAAACTTCCGCCAGATCTCACCTCTC 182
DB 121 GCTCTCGCAACCGCTGGAGTTATGATTTCTCTCAAAAACTTCCGCCAGATCTCACCTCTC 180
QY 183 GTTCAACTCATCTCAAGCAGGTGTACCTTACGCTATACCTGTGCTTTAGTGGCATCGGCT 242
DB 181 GTTCAACTCATCTCAAGCAGGTGTACCTTACGCTATACCTGTGCTTTAGTGGCATCGGCT 240
QY 243 GCTGGGCTTACCTTCAATTCATGGAATATCGGTGGCTTCTTCAACAATGGCTTGC 302
DB 241 GCTGGGCTTACCTTCAATTCATGGAATATCGGTGGCTTCTTCAACAATGGCTTGC 300
QY 303 ATGGGAAGCATGTGTGGCTTCTCTCAGCTCCTCTTATCAAGAGCAAAAAGGTTGGCT 362
DB 301 ATGGGAAGCATGTGTGGCTTCTCTCAGCTCCTCTTATCAAGAGCAAAAAGGTTGGCT 360
QY 363 CTCTCTGATGGAGCTGCACCTTTTGAAGCGCTCTATGTCCTCTGATTCAGTGGGCT 422
DB 361 CTCTCTGATGGAGCTGCACCTTTTGAAGCGCTCTATGTCCTCTGATTCAGTGGGCT 420
QY 423 ATTAACCTTCGATCCAGCATTTGTTTGGCGCTTTTGTAGGTTGTGCTGTGTTTGGT 482
DB 421 ATTAACCTTCGATCCAGCATTTGTTTGGCGCTTTTGTAGGTTGTGCTGTGTTTGGT 480
QY 483 TGCTTCTCAGCTGCTGCCAATGTGGCAAGCGCGCTCTATGTCCTCTGATTCAGTGGGCT 542
DB 481 TGCTTCTCAGCTGCTGCCAATGTGGCAAGCGCGCTCTATGTCCTCTGATTCAGTGGGCT 540
QY 543 CTCTCATCTGGGCTCTCCCTTCTCTTCGTTGTCACCTTTCATCTCCATTTTTCGTTGGT 602
DB 541 CTCTCATCTGGGCTCTCCCTTCTCTTCGTTGTCACCTTTCATCTCCATTTTTCGTTGGT 600
QY 603 TCCATGGCTGTTTTCAAGTTGAGTTGATTTTGGACTCTTGG 645
DB 601 TCCATGGCTGTTTTCAAGTTGAGTTGATTTTGGACTCTTGG 643

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RESULT 4
AW219279 646 bp mRNA linear EST 18-MAY-2001
LOCUS EST301761 tomato root during/after fruit set, Cornell University
DEFINITION Lycopersicon esculentum cDNA clone cLEX3N8, mRNA sequence.
ACCESSION AW219279
VERSION AW219279.1 GI:6530153
KEYWORDS tomato.
SOURCE Lycopersicon esculentum
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE
1 (bases 1 to 646)
van der Hoeven, R.S., Garvin, D., Matern, A.L., Holt, I.E., Liang, F.,
Upton, J., Hansen, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M.,
Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.
Generation of ESTs from tomato root tissue
Unpublished (1999)
CONTACT: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES
source
Location/Qualifiers
1..646
/organism="Lycopersicon esculentum"

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/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEX3N8"
/clone_lib="tomato root during/after fruit set, Cornell University"
/tissue_type="root"
/dev_stage="plants during and after fruit-set"
/note="vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; supplier: Tanksley; Tissue supplied by Dave Garvin (USDA-ARS, Ithaca, NY 14850)."
BASE COUNT 131 a 155 c 151 g 209 t
ORIGIN

Query Match 61.3%; Score 634; DB 10; Length 646;
Best Local Similarity 99.8%; Pred. No. 7.8e-152;
Matches 645; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 GAGCAAAACATACATGCTAGCTTCAGATAAATATCTTTGCTCATTTTCAGTTCACAAA 60
DB 1 GAGCAAAACATACATGCTAGCTTCAGATAAATATCTTTGCTCATTTTCAGTTCACAAA 60
QY 61 ACTCGAAG 120
DB 61 ACTCGAAG 120
QY 121 CTGCTCTCTCGCAACCGCTGGAGTATGATTTCTCTCAAAAATCTTCGCGAGATCTCACCTC 180
DB 121 CTGCTCTCTCGCAACCGCTGGAGTATGATTTCTCTCAAAAATCTTCGCGAGATCTCACCTC 180
QY 181 TGTTCAAACTCATCTCAAGAGAGGTACCTAGCTATGCTGTGCTTTAGTGGCATCGG 240
DB 181 TGTTCAAACTCATCTCAAGAGAGGTACCTAGCTATGCTGTGCTTTAGTGGCATCGG 240
QY 241 CTGCTGGGCTTACCTTCACATTTCTATGAATATCGGTGGCTCTCTCACAAACATGCTTT 300
DB 241 CTGCTGGGCTTACCTTCACATTTCTATGAATATCGGTGGCTCTCTCACAAACATGCTTT 300
QY 301 GATGGGAAGAGTGTGTGCTTCTCTAGCTCTCTCTTATCAAGAGAGAGAGAGAGAGAG 360
DB 301 GATGGGAAGAGTGTGTGCTTCTCTAGCTCTCTCTTATCAAGAGAGAGAGAGAGAGAG 360
QY 361 CTCTCTGATGCGAGCTGCACATTTTGAAGGCGCTCTATTGCTCTCTGATGAGCTGG 420
DB 361 CTCTCTGATGCGAGCTGCACATTTTGAAGGCGCTCTATTGCTCTCTGATGAGCTGG 420
QY 421 GCATTAACCTCGATCCAGCATTTGTGTGGGCTTTTGTAGGTTGTGCTGTGTTTTTG 480
DB 421 GCATTAACCTCGATCCAGCATTTGTGTGGGCTTTTGTAGGTTGTGCTGTGTTTTTG 480
QY 481 GTTGCTTCTCAGCTGCTGCATGTTGGCAAGCGCAGGAGTACTTGTACCTCGGGGCC 540
DB 481 GTTGCTTCTCAGCTGCTGCATGTTGGCAAGCGCAGGAGTACTTGTACCTCGGGGCC 540
QY 541 TTCTTTTCACTGGCGTCTCCCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 541 TTCTTTTCACTGGCGTCTCCCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
QY 601 GTTCCATGCTGTTTTTCAAGTTGAGTTGATTTTGGACTCTTGG 645
DB 601 GTTCCATGCTGTTTTTCAAGTTGAGTTGATTTTGGACTCTTGG 646

RESULT 5
LOCUS BG127849 647 bp mRNA linear EST 31-JAN-2001
DEFINITION EST473495 tomato shoot/meristem Lycopersicon esculentum cDNA clone
ACCESSION EF01888 5' sequence, mRNA sequence.
VERSION BG127849
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 647)
van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Utterback,T.,
Hansen,C., Ronning,C. and Tanksley,S.
Generation of ESTs from tomato shoot/meristem tissue
Unpublished (2001)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>.
FEATURES
Location/Qualifiers
1..647
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cTOF18B8"
/clone_lib="tomato shoot/meristem"
/tissue_type="shoot/meristem"
/dev_stage="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; Small expanding leaves from the growing tip were
taken from greenhouse plants (4-6wks old TA496). Tissue
was immediately frozen in liquid nitrogen."
BASE COUNT 129 a 154 c 153 g 211 t
ORIGIN

Query Match 60.1%; Score 621.8; DB 12; Length 647;
Best Local Similarity 98.6%; Pred. No. 1e-148; 7; Indels 2; Gaps 1;
Matches 638; Conservative 0; Mismatches 7;
QY 3 GCAACATACATTTGCTAGCTTCAGATAAATATCTTTGCTCATTTTCAGTTCACAAAAC 62
DB 1 GCAACATACATTTGCTAGCTTCAGATAAATATCTTTGCTCATTTTCAGTTCACAAAAC 60
QY 63 TCGAAG 122
DB 61 TCGAAG 120
QY 123 GCCTCTCGCAACCGCTGGAGTATGATTTCTCTCAAAAATCTTCGCGAGATCTCACCTCTC 182
DB 121 GCCTCTCGCAACCGCTGGAGTATGATTTCTCTCAAAAATCTTCGCGAGATCTCACCTCTC 180
QY 183 GTTCAAACCTCATCTCAAGCAGGTGATCTTACGCTATGCTGTCTTTAGTGGCATCGGCT 242
DB 181 GTTCAAACCTCATCTCAAGCAGGTGATCTTACGCTATGCTGTCTTTAGTGGCATCGGCT 240
QY 243 GCTGGGGCTTACCTTTCACATTTCTATGAATATCGGTGGCTCTCTCAACAATGCTTTC 302
DB 241 GCTGGGGCTTACCTTTCACATTTCTATGAATATCGGTGGCTCTCTCAACAATGCTTTC 300
QY 303 ATGGGAACATGTTGGCTTCTCTCAGCTCTCTCTTATCAAGAGAGAGAGAGAGAGAG 362
DB 301 ATGGGAACATGTTGGCTTCTCTCAGCTCTCTCTTATCAAGAGAGAGAGAGAGAGAG 360
QY 363 CTTCGTAGGCGAGCTGCACATTTTGAAGGCGCTCTATTTGGTCTCTCTGATTGAGCTGGGC 422
DB 361 CTTCGTAGGCGAGCTGCACATTTTGAAGGCGCTCTATTTGGTCTCTCTGATTGAGCTGGGC 420
QY 423 ATTAACCTCGATCCAGCATTTGTTGGGCGCTTTTGTAGTTGTGCTGTGTTTTTGGT 482
DB 421 ATTAACCTCGATCCAGCATTTGTTGGGCGCTTTTGTAGTTGTGCTGTGTTTTTGGT 480
QY 483 TCGTCTCTCAGCTGCTGCCAUGTTGGCAAGCGCAGGAGTACTTGTACCTCGGGGGCCTT 542
DB 481 TCGTCTCTCAGCTGCTGCCAUGTTGGCAAGCGCAGGAGTACTTGTACCTCGGGGGCCTT 540
QY 543 CTTCATCTGGGCTCTCCCTCTCTCTCTGTTGCACTTTCATCTCCATCTTTTGG--TG 600
DB 541 CTTCATCTGGGCTCTCCCTCTCTCTCTGTTGCACTTTCATCTCCATCTTTTGGGTGG 600

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QY 601 GTTCCATGGCTGTTTCAAGTTTGAGTTGATTTTGGACTCTTGTTGGT 647
Db 601 TTCCATGGGCTGTTTCAAGTTTGAGTTGATTTTGGACTCTTGTTGGT 647

RESULT 6
AI779122 AI779122 596 bp mRNA linear EST 18-MAY-2001
LOCUS EST260001 tomato susceptible, Cornell Lycopersicon esculentum cDNA
DEFINITION
ACCESSION AI779122
VERSION AI779122
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 596)
AUTHORS D'Ascenzo M., He X., Lyman J., Matern A.L., Vision T., Holt, I.E.,
Liang F., Upton J., Roming C.M., Craven M.B., Fujii C.Y., Bowman
C.L., Nierman W., Fraser C.M., Venter J.C., Tanksley S.D.,
Giovannoni J.J. and Martin G.B.
TITLE Generation of ESTs from Pseudomonas susceptible tomato
JOURNAL Unpublished (1999)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES
source
1..596
/organism="Lycopersicon esculentum"
/cultivar="R11-13 (Rio Grande x Money Maker)"
/db_xref="taxon:4081"
/clone="CL57M13"
/clone_lib="tomato susceptible, Cornell"
/tissue_type="leaf"
/dev_stage="4-week old"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; CL5 - Tomato Pseudomonas Susceptible EST Library.
Directionally cloned cDNAs inserted into pBluescript SK(-)
at 5' end with EcoRI and 3' end with XhoI site"
BASE COUNT 102 a 140 c 150 g 204 t
ORIGIN
Query Match 57.6%; Score 596; DB 9; Length 596;
Best Local Similarity 100.0%; Pred. No. 4.3e-142; Indels 0; Gaps 0;
Matches 596; Conservative 0; Mismatches 0;
QY 161 CTTCCGCGAGATCTCACCTCTCGTTCAAACCTATCTCAAGCAGGTGTACCTTACGCTATG 220
Db 1 CTTCCGCGAGATCTCACCTCTCGTTCAAACCTATCTCAAGCAGGTGTACCTTACGCTATG 60
QY 221 CTGTGCTTTAGTGCATCGGCTGCTGGGCTTACCTTCAATCTATGAATATCGTGG 280
Db 61 CTGTGCTTTAGTGCATCGGCTGCTGGGCTTACCTTCAATCTATGAATATCGTGG 120
QY 281 CCTCTCACACAAATGCTTGATGGAAGCATGGTGTGGCTTCTCTCAGCTCCCTCTTA 340
Db 121 CCTCTCACACAAATGCTTGATGGAAGCATGGTGTGGCTTCTCTCAGCTCCCTCTTA 180
QY 341 TCAAGAGCAAAAAGGTGGCTTCTGTATGGAGCTGCATCTTATGAAGGGCGCTCTAT 400
Db 181 TCAAGAGCAAAAAGGTGGCTTCTGTATGGAGCTGCATCTTATGAAGGGCGCTCTAT 240
QY 401 TGGTCTCTGATTCAGCTGGGCATTAATCTCGATCCAAAGCATTTGTTGGGCTTTTGT 460
Db 241 TGGTCTCTGATTCAGCTGGGCATTAATCTCGATCCAAAGCATTTGTTGGGCTTTTGT 300

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QY 461 AGTTTGTCTGTGGTTTGTGTTTCTCAGCTGCTGCCATGTTGGCAAGCGCAGGGA 520
Db 301 AGTTTGTCTGTGGTTTGTGTTTCTCAGCTGCTGCCATGTTGGCAAGCGCAGGGA 360
QY 521 GTACTTGTACCTCGGGGGCCCTTCTTTTCATCTGGGCTCTCCCTTCTCTCGTTGCATT 580
Db 361 GTACTTGTACCTCGGGGGCCCTTCTTTTCATCTGGGCTCTCCCTTCTCTCGTTGCATT 420
QY 581 TGCATCCTCCATTTTGTGGTTCATGCTGTTTTCAGTTTGAAGTTTGAAGTTTGAAGTT 640
Db 421 TGCATCCTCCATTTTGTGGTTCATGCTGTTTTCAGTTTGAAGTTTGAAGTTTGAAGTT 480
QY 641 CTTGGTGTGGGCTACATGCTCTTTTGACACCAAGAAATTTGAGAAGGCTCACTT 700
Db 481 CTTGGTGTGGGCTACATGCTCTTTTGACACCAAGAAATTTGAGAAGGCTCACTT 540
QY 701 GGGTGATATGATAGTTTAAAGCATGCAATGACCTTTTTCAGATTTTGGCGTG 756
Db 541 GGGTGATATGATAGTTTAAAGCATGCAATGACCTTTTTCAGATTTTGGCGTG 596

RESULT 7
EG134507
LOCUS EST467399 tomato crown gall Lycopersicon esculentum cDNA clone
DEFINITION
ACCESSION EG134507
VERSION EG134507.1 GI:12634695
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 592)
AUTHORS van der Hoeven R., Sun H., Cho J., Utterback T., Hansen C., Ronning
C. and Tanksley S.
TITLE Generation of ESTs from tomato crown gall tissue
JOURNAL Unpublished (2001)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
1..592
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cTOE18F5"
/tissue_type="crown gall"
/dev_stage="crown galls from full-grown plants (8 wks old)"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; Four wk old greenhouse plants were stab inoculated
on stem with Agrobacterium tumefaciens C58 (Dr. I.J. Burr,
Cornell U.). Galls were allowed to develop for another 4
wks, when gall tissue was frozen in liquid nitrogen."
BASE COUNT 123 a 149 c 135 g 184 t
ORIGIN
Query Match 57.2%; Score 591; DB 12; Length 592;
Best Local Similarity 99.8%; Pred. No. 8.1e-141; Indels 0; Gaps 0;
Matches 591; Conservative 0; Mismatches 1;
QY 3 GCAACATACATTTGCTACGTTCAGATAAATATCCTTTGCTCATTTCAAGTTCCAAAAC 62
Db 1 GCAACATACATTTGCTACGTTCAGATAAATATCCTTTGCTCATTTCAAGTTCCAAAAC 60

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QY 63 TCGAAGAAAGAAAGAGAGAAACAATGGAAGGTTTCACATGTTCTTCGACTCGCAATCT 122
DB 61 TCGAAGAAAGAAAGAGAGAGAAACAATGGAAGGTTTCACATGTTCTTCGACTCGCAATCT 120
QY 123 GCCTCTCCAAACCGGTGAGTATGATGATCTCTCAAAACTTCGCCAGATCTCACCTTC 182
DB 121 GCCTCTCCAAACCGGTGAGTATGATGATCTCTCAAAACTTCGCCAGATCTCACCTTC 180
QY 183 GTTCAAACTCATCTCAAGCAGGTGTACCTTACGCTATGCTGTCTTTAGTGGCATCGGCT 242
DB 181 GTTCAAACTCATCTCAAGCAGGTGTACCTTACGCTATGCTGTCTTTAGTGGCATCGGCT 240
QY 243 GCTGGGCTTACCTTCAATCTATGGAATATCGGTGGCTCTCCACAAACAATGGCTTTC 302
DB 241 GCTGGGCTTACCTTCAATCTATGGAATATCGGTGGCTCTCCACAAACAATGGCTTTC 300
QY 303 ATGGGAAGCATGGTGTGGCTCTCTCAGCTCTCTCTTATCAAGAGCAAAAAGGGTGGCT 362
DB 301 ATGGGAAGCATGGTGTGGCTCTCTCAGCTCTCTCTTATCAAGAGCAAAAAGGGTGGCT 360
QY 363 CTTCTGATGGCAGCTGCACTTTTGAAGGGCGCTCTATGCTCTCTGATGAGCTGGGC 422
DB 361 CTTCTGATGGCAGCTGCACTTTTGAAGGGCGCTCTATGCTCTCTGATGAGCTGGGC 420
QY 423 ATTAATCTCGATCCAGCAATGCTGTTTGGCGCTTTTGTAGTGTGCTGTGGTGTGTTTGGT 482
DB 421 ATTAATCTCGATCCAGCAATGCTGTTTGGCGCTTTTGTAGTGTGCTGTGGTGTGTTTGGT 480
QY 483 TGTCTTCAAGCTGCTGCCATGTTGCAAGGGCGCAGGAGTACTTGTATCTCGGGGGCCTT 542
DB 481 TGTCTTCAAGCTGCTGCCATGTTGCAAGGGCGCAGGAGTACTTGTATCTCGGGGGCCTT 540
QY 543 CTTTCACTTGGGGTCTCCCTCTCTCTGTTTGGCACTTTGCACTCTCCATTT 594
DB 541 CTTTCACTTGGGGTCTCCCTCTCTCTGTTTGGCACTTTGCACTCTCCATTT 592

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RESULT 8
BQ115430 578 bp mRNA linear EST 22-JUL-2002
LOCUS EST600993 mixed potato tissues Solanum tuberosum cDNA clone STMDA93
DEFINITION 5' end, mRNA sequence.
ACCESSION BQ115430
VERSION BQ115430.2 GI:21916950
KEYWORDS EST.
SOURCE potato.

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ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C.,
Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and
Karamycheva, S.A.
Generation of a set of potato cDNA clones for microarray analyses
Unpublished (2002)
On Apr 17, 2002 this sequence version replaced gi:20167379.
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato@igr.org
This clone is available through the Research Genetics, contact the
Research Genetics for further information 1-800-711-6195 or
cnaresgen.com
Seq primer: 13.
Location/Qualifiers
1. .578
/organism="Solanum tuberosum"
/cultivar="Kennebec or Binjite"
/db xref="taxon.4113"
/clone="STMDA93"
/clone_lib="mixed potato tissues"
/tissue_type="mixed tissues"

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FEATURES

source

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/lab_host="SOLR"
/Note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Combination of untreated and Phytophthora
infestans-treated libraries of stolons, leaves, leaflets,
axillary buds of stem explants, petioles, germinating eyes
tubers, or roots."

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BASE COUNT 117 a 140 c 137 g 184 t
ORIGIN

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Query Match 51.7%; Score 534.2; DB 14; Length 578;
Best Local Similarity 96.5%; Pred. No. 3e-126;
Matches 557; Conservative 0; Mismatches 18; Indels 2; Gaps 1;

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QY 11 AACATCTCTACGTTACAGATAAATATCCTTTTGCTCATTTTCAGTTCCTCAAAAACCTCGAAGAA 70
DB 4 AACATTTGTACGTTACAGATAAATATCCTTTTGCTCGTTTCAGTTCCTCAAAAACCTCGAAGAA 63
QY 71 GAAGAAGAAGAGAACAAATGAAGGTTTCACATGTTCTTCGACTCGCAATCTGCTCTCG 130
DB 64 GAAGAAGA--AGAAATATGAGGGTTTCACATGTTCTTCGACTCGCAATCTGCTCTCG 121
QY 131 CAACGGTGGAGTTATGATTTCTCTCAAAAACCTTCGCCAGATCTCACCTCTCGTTCAAAAC 190
DB 122 CAACGGTGGAGTTATGATTTCTCTCAAGAATCTTCGCCAGATCTCACCTCTCGTTCAAAAC 181
QY 191 TCATCTCAAGCAGGTGTACCTTACGCTATGCTGTGTTTAGTGGCATCGGCTGCTGGGC 250
DB 182 TCATCTCAAGCAGGTGTACCTTACGCTATGCTGTGTTTAGTGGCATCGGCTGCTGGGC 241
QY 251 TTACCTTCACATCTATGGAATATCGGTGGCTCTCCACAAACAATGGCTTGCAATGGGAAG 310
DB 242 TTACCTTCACATCTATGGAATATCGGTGGCTCTCCACAAACAATGGCTTGCAATGGGAAG 301
QY 311 CATGTGTGGCTTCTCTCAGCTCTCTCTTATCAAGAGCAAAAAGGGTGGCTTCTCTGAT 370
DB 302 CATGTGTGGCTTCTCTCAGCTCTCTCTTATCAAGAGCAAAAAGGGTGGCTTCTCTGAT 361
QY 371 GCAGCTGCATTTTGAAGGGCTCTATTTGCTCTGCTCATTTGAGCTGGGCATTAACCT 430
DB 362 GCAGCTGCATTTTGAAGGGCTCTCTATTTGCTCTGCTCATTTGAGCTGGGCATTAACCT 421
QY 431 CGATCCAAAGCATTTGTTTGGCGCTTTTGTAGTGTGCTGTGTTTGGTGTGCTTCTC 490
DB 422 CGATCCAAAGCATTTGTTTGGCGCTTTTGTAGTGTGCTGTGTTTGGTGTGCTTCTC 481
QY 491 AGCTCTGCCATTTGGAAGCGCAGGAGTACTTCTACCTCGGGGGCCTTCTTTCATC 550
DB 482 AGCTCTGCCATTTGGAAGCGGAGGAGTACTTGTACCTCGGGGGCCTTCTTTCATC 541
QY 551 TGGCGTCTCCCTTCTCTCTCTGTTGCACTTTGCACTCC 587
DB 542 TGGTGTCTCCCTTCTCTCTCTGTTGCACTTGGCATCC 578

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RESULT 9
BF054243 540 bp mRNA linear EST 16-OCT-2000
LOCUS EST439473 potato leaves and petioles Solanum tuberosum cDNA clone
DEFINITION cSTB39K21.5' sequence, mRNA sequence.
ACCESSION BF054243
VERSION BF054243.1 GI:10808139
KEYWORDS EST.
SOURCE potato.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 540)
van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J.,
Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Roming,
C.M., Fry, W.B., Tanksley, S.D. and Baker, B.
Generation of ESTs from potato leaves and petioles
Unpublished (2000)

```

COMMENT

Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com.
Location/Qualifiers

FEATURES

source
1. .540
/organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTB39K21"
/clone_lib="potato leaves and petioles"
/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"
/note="vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; Tissue was supplied by Dr. Fry (Cornell University).
Leaflets and petioles were isolated from 8 week old
greenhouse grown plants. The plants were watered and
fertilized freely. The tissue was immediately frozen in
liquid nitrogen."
BASE COUNT 114 a 127 c 130 g 169 t
ORIGIN

Query Match 48.2%; Score 498.4; DB 12; Length 540;
Best Local Similarity 96.5%; Pred. No. 4.5e-117;
Matches 521; Conservative 0; Mismatches 16; Indels 3; Gaps 1;
QY 11 AACATTGCTAGGTCAGATAAATATCCTTTGCTCATTTCAGTTCGAAAACTCGAAGAA 70
DB 4 AACATTGCTAGGTCAGATAAATATCCTTTGCTCATTTCAGTTCGAAAACTCGAA 60
QY 71 GAAGAAGAAGAACAAATGGAAGGTTTCACATCGTTCTTCGATCGCAATCTGCCCTCTCG 130
DB 61 GAAGAAGAAGAAATATGAGGGTTTCACATCGTTCTTCGATCGCAATCTGCCCTCTCG 120
QY 131 CAACCGTGGAGTTATGATTTCTTCAAAAATTCGCGCAGATCTCACTCTGTTCAAAAC 190
DB 121 CAACCGTGGAGTTATGATTTCTTCAAAAATTCGCGCAGATCTCACTCTGTTCAAAAC 180
QY 191 TCATCTCAAGCAGGTGTACCTTACGCTATGCTGTGCTTTAGTGGCATCGGCTCTCGGCG 250
DB 181 TCATCTCAAGCAGGTGTACCTTACGCTATGCTGTGCTTTAGTGGCATCGGCTCTCGGCG 240
QY 251 TTACCTTCACATTTCTATGGAATATCGGTGGCCTCTTCAACAATGCTTTGCAATGGAAG 310
DB 241 TTACCTTCACATTTCTATGGAATATCGGTGGCCTCTTCAACAATGCTTTGCAATGGAAG 300
QY 311 CATGTTGGCTTCTCTCAGCTCTCTTATCAAGACAAAGGGTGGCTCTTCTGAT 370
DB 301 CATGTTGGCTTCTCTCAGCTCTCTTATCAAGACAAAGGGTGGCTCTTCTGAT 360
QY 371 GGCAGCTGCATTTTGAAGCGCCTCTATTTGGTCTCTGATTGAGCTGGGCATTAACTT 430
DB 361 GGCAGCTGCATTTTGAAGCGCCTCTATTTGGTCTCTGATTGAGCTGGGCATTAACTT 420
QY 431 CGATCCAGCATTTGTTGGCGCTTTTGTAGTTGCTGTGGTTTGGTTGCTTCTC 490
DB 421 CGATCCAGCATTTGTTGGCGCTTTTGTAGTTGCTGTGGTTTGGTTGCTTCTC 480
QY 491 AGCTGCTGCCATTTGGCAAGCGCAGGAGTACTTGTACTCGGGGCGCTTCTTTTCATC 550
DB 481 AGCTGCTGCCATTTGGCAAGCGTAGGAGTACTTGTACTCGGGGCGCTTCTTTTCATC 540

RESULT 10

BI935239
LOCUS BI935239 476 bp mRNA linear EST 18-OCT-2001
DEFINITION EST55128 tomato flower, anthesis Lycopersicon esculentum cDNA
clone cTOD22C8 5' end, mRNA sequence.
ACCESSION BI935239
VERSION BI935239.1 GI:16249711
KEYWORDS EST.
SOURCE tomato.

ORGANISM

Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 476)

REFERENCE

AUTHORS
van der Hoeven,R.S., Bezzerides,J.L., Karamycheva,S.A., Tsai,J.,
Utterback,T., Van Aken,S., Ronning,C.M., Nierman,W., Fraser,C.M.,
Martin,G.B., Giovannoni,J.J. and Tanksley,S.D.
Generation of ESTs from tomato flower tissue, anthesis (2001)
Unpublished (2001)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
This clone is available through the Clemson University Genomics
Institute

TITLE

JOURNAL

COMMENT

FEATURES

source
1. .476
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cTOD22C8"
/clone_lib="tomato flower, anthesis"
/tissue_type="flower"
/dev_stage="anthesis"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Cornell University; sequencing: The
Institute for Genomic Research; Flower buds and flowers
were taken from greenhouse plants (4-8 wks old, TA496).
They were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
BASE COUNT 114 a 115 c 106 g 141 t
ORIGIN

Query Match 45.3%; Score 468.8; DB 13; Length 476;
Best Local Similarity 99.6%; Pred. No. 1.7e-109;
Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 AGCAACATCAATTTGCTACGTTTCAGATAAATATCCTTTGCTCATTTCAGTTCGAAAAA 61
DB 5 AGCAACATCAATTTGCTACGTTTCAGATAAATATCCTTTGCTCATTTCAGTTCGAAAAA 64
QY 62 CTCAAGAAAGAAAGAGAACAAATGGAAGTTTCACATCGTTCTTCGACTCGCAATC 121
DB 65 CTCAAGAAAGAGAGAACAAATGGAAGTTTCACATCGTTCTTCGACTCGCAATC 124
QY 122 TGCCTCTCGCAACCGCTGGAGTTATGATTCTCTCAAAAACCTTCGCGCAGATCTCACCTCT 181
DB 125 TGCCTCTCGCAACCGCTGGAGTTATGATTCTCTCAAAAACCTTCGCGCAGATCTCACCTCT 184
QY 182 CGTTCAAACTCATCTCAAGCAGGTGTACCTTACGCTATGCTGTGTTAGTGGCATCGGC 241
DB 185 CGTTCAAACTCATCTCAAGCAGGTGTACCTTACGCTATGCTGTGTTAGTGGCATCGGC 244
QY 242 TGCCTGGGGCTTACCTTCACATTCTATGGAATATCGGTGGCCTCTCAACAACATGCGCTTG 301
DB 245 TGCCTGGGGCTTACCTTCACATTCTATGGAATATCGGTGGCCTCTCAACAACATGCGCTTG 304
QY 302 CATGGGAAGCATGGTGTGGCTTCTCTCAGCTCTCTTATCAAGAGCAAAAAGGGTGGC 361
DB 305 CATGGGAAGCATGGTGTGGCTTCTCTCAGCTCTCTTATCAAGAGCAAAAAGGGTGGC 364
QY 362 TCTTCTCATGGCAGCTGCACCTTTTGAAGCGCGCTCTATTGGTCTCTGATTGAGCTGGG 421
DB 365 TCTTCTCATGGCAGCTGCACCTTTTGAAGCGCGCTCTATTGGTCTCTGATTGAGCTGGG 424
QY 422 CATTAACCTTCATCCAGCATTTGCTTTGGCGCTTTTGTAGCTTGTGCTGTG 473
DB 425 CATTAACCTTCATCCAGCATTTGCTTTGGCGCTTTTGTAGCTTGTGCTGTG 476

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RESULT 11
AI895377      464 bp  mRNA  linear  EST 18-MAY-2001
LOCUS      EST264820 tomato callus, TAMU Lycopersicon esculentum cDNA clone
DEFINITION cLEC7H19, mRNA sequence.
ACCESSION  AI895377
VERSION    AI895377.1 GI:5601279
KEYWORDS   EST.
SOURCE     tomato.
ORGANISM   Lycopersicon esculentum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
            Lycopersicon.
REFERENCE  1 (bases 1 to 464)
AUTHORS   Alcalá, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E.,
            Liang, F., Upton, J., Craven, M.B., Bowman, C.L., Ann, S., Romling,
            C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
            Generation of ESTs from tomato callus tissue
            Unpublished (1999)
COMMENT   Contact: CUGI
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Email: http://www.genome.clemson.edu/orders/index.html
            5 prime sequence.
FEATURES             Location/Qualifiers
     source           1..464
                     /organism="Lycopersicon esculentum"
                     /cultivar="TA496"
                     /db_xref="taxon:4081"
                     /clone_lib="tomato callus, TAMU"
                     /tissue_type="callus"
                     /dev_stage="25-40 days old"
                     /lab_host="XLI-Blue MRP"
                     /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
                     XhoI; supplier: Giovannoni laboratory; CLEC - Cotyledons
                     of seedlings 7-10 days post-germination were excised, cut
                     at both ends and placed on MS medium with no selection.
                     Mixed callus was harvested at 25 and 40 days and included
                     undifferentiated masses. Tomato Callus EST Library"
BASE COUNT          99 a 112 c 116 g 137 t
ORIGIN
Query Match      43.9%; Score 454.4; DB 9; Length 464;
Best Local Similarity 98.7%; Pred. No. 8.3e-106;
Matches 458; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 62 CTCGAAGAAGAGAAGAGAAGACATGATGAGGTTTCATCGTTCTTCGACTCGCAATC 121
DB 1 CTCGAAGAAGAGAAGAGAAGATCAATGAGGTTTCATCGTTCTTCGACTCGCAATC 60
QY 122 TGCCTCTCGAACCGTGGAGTATGATTTCTCAAAACATTCGCCAGATCCACCTCT 181
DB 61 TGCCTCTCGAACCGTGGAGTATGATTTCTCAAAACATTCGCCAGATCCACCTCT 120
QY 182 CGTTCAAACATCATCTCAAGCAGGTGTACCTTACGCTATCGTGTCTTTAGTGGCATCGGC 241
DB 121 CGTTCAAACATCATCTCAAGCAGGTGTACCTTACGCTATCGTGTCTTTAGTGGCATCGGC 180
QY 242 TCGTGGGCTTACCTTCACATTCATGGAATATCGGTGGCTTCCTCAACAAGATGGCTTG 301
DB 181 TCGTGGGCTTACCTTCACATTCATGGAATATCGGTGGCTTCCTCAACAAGATGGCTTG 240
QY 302 CATGGGAAGCATGGTGGGCTTCTCTCAGCTCCTCCTTATCAAGAGCAAAAAGGGTGGC 361
DB 241 CATGGGAAGCATGGTGGGCTTCTCTCAGCTCCTCCTTATCAAGAGCAAAAAGGGTGGC 300
QY 362 TCTTCTGATGGAGCTGCACATTTTGAAGCGGCTCTATGTCTCTCATGAGCTGG 421
DB 301 TCTTCTGATGGAGCTGCACATTTTGAAGCGGCTCTATGTCTCTCATGAGCTGG 360

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QY 422 CATTAACTTCGATCCCAAGCATGTGTTTGGCGCTTTTGTAGTGTGTGCTGTTTGG 481
DB 361 CATTAACCTTCGATCCCAAGCATGTGTTTGGCGCTTTTGTAGTGTGTGTTATGG 420
QY 482 TTGCTTCTCAGCTGCTGCCATGTGTGCAAGGCGCAGGAGTACT 525
DB 421 TTGCTTCTCAACTGCTGGCATGTGTGCAAGGCGCAGGAGTACT 464

RESULT 12
BQ115431/c 617 bp  mRNA  linear  EST 17-APR-2002
LOCUS      EST600994 mixed potato tissues Solanum tuberosum cDNA clone STMDA93
DEFINITION 3' end, mRNA sequence.
ACCESSION  BQ115431
VERSION    BQ115431.1 GI:20167380
KEYWORDS   EST.
SOURCE     potato.
ORGANISM   Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE  1 (bases 1 to 617)
AUTHORS   Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C.,
            Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and
            Karanycheva, S.A.
            Generation of a set of potato cDNA clones for microarray analyses
            Unpublished (2002)
COMMENT   Contact: Robin Buell
            The Institute for Genomic Research
            9712 Medical Center Dr, Rockville, MD 20850, USA
            Email: potato@igr.org
            This clone is available through the Research Genetics, contact the
            Research Genetics for further information 1-800-711-6195 or
            cdna@resgen.com
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source           1..617
                     /organism="Solanum tuberosum"
                     /cultivar="Kennebec or Binjite"
                     /db_xref="taxon:4113"
                     /clone="STMDA93"
                     /clone_lib="mixed potato tissues"
                     /tissue_type="mixed tissues"
                     /lab_host="SOLR"
                     /note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
                     XhoI; supplier: Combination of untreated and Phytophthora
                     infestans-treated libraries of stolons, leaves, leaflets,
                     axillary buds of stem explants, petioles, germinating eyes
                     , tubers, or roots."
BASE COUNT          219 a 152 c 114 g 132 t
ORIGIN
Query Match      43.4%; Score 449.2; DB 14; Length 617;
Best Local Similarity 89.9%; Pred. No. 1.9e-104;
Matches 524; Conservative 0; Mismatches 34; Indels 25; Gaps 3;
QY 402 GGTCTCTGATGAGCTGGCATTAACTTCATCTCGACTGCTGCCATGTGGCAAGCGGTAGGGA 460
DB 617 GGTCTCTGATGAGCTGGCATTAACTTCATCTCGACTGCTGCCATGTGGCAAGCGGTAGGGA 558
QY 461 AGGTTGTGTGTGGTGTGTTTGTGTTGTTCTCAGCTGCTGCCATGTGGCAAGCGCGCAGGA 520
DB 557 AGGTTGTGTGTGGTGTGTTTGTGTTGTTCTCAGCTGCTGCCATGTGGCAAGCGGTAGGGA 498
QY 521 GTACTGTGACCTCGGGGGCTTCTTTCATCTGCGGTCTCCCTTCTCTTCTGTTGCACTT 580
DB 497 GTACTGTGACCTCGGGGGCTTCTTTCATCTGCGGTCTCCCTTCTCTTCTGTTGCACTT 438
QY 581 TGCATCTCCTCATTTTGTGGTTCATCGCTGTTTCAAGTTTCAGTTTCAGTTTCAGTTTCAGCT 640
DB 437 CGCATCTCCATTTTGTGGTTCATCGCTGTTTCAAGTTTCAGTTTCAGTTTCAGTTTCAGCT 378

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QY 641 CTTGGTGTGTTGGGCTACATGCTCTTGGACCCCAAGAAATATTGAGAGGCTCACTT 700
DB 377 CTTGGTGTGTTGGGCTACATGCTCTTGGACCCCAAGAAATATTGAGAGGCTCACTT 318
QY 701 GGGTGATATGGAATACGTTAAGCATGCAATGACCTTTTTCACAGATTTTGGCGCTGTTTT 760
DB 317 GGGTGATATGGAATACGTTAAGCATGCTTTGACCTCTTTCACAGATTTTGGCTGTTTT 258
QY 761 TGTGCGGATCTGATCATCATGTTAAAGTAATGATCTGAGAGGAGAGAGAGAGAA 820
DB 257 TGTGCGGATCTGATCATCATGTTAAAGTAATGATCTGAGAGGAGAGAGAGAGAA 198
QY 821 GAGGAGAACTAGATTTGCTTCT- - - - - CAACTTGTGTTTCCANA 861
DB 197 GAGGAGAACTAGATTTGCTTCTATGGGCTACTGGGACTCTAACCTGTGTTTTCATA 138
QY 862 ACTCCTTGTGTTCACTGAAACAGCATGTTAATAGTTGATCTTCTTCACTTTAGCA 921
DB 137 ATACACTGTGTTCACTGAAACAGCATGTTAATAGTTGATCTTCTTCACTTTAGCA 83
QY 922 TAGGCTGTGATGTAATGCTGTGACATGCCATTATGGCTGTG 964
DB 82 TTGGCTGTGATACATAATCTGTGGACATGCCATTATGGCTGTG 40

RESULT 13
AW399750 456 bp mRNA linear EST 18-MAY-2001
LOCUS EST257641 tomato resistant, Cornell Lycopersicon esculentum cDNA
DEFINITION clone cLER18J18, mRNA sequence.
ACCESSION AW399750
VERSION AW399750.1 GI:5274582
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 456)
AUTHORS D'Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E.,
Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman
C.L., Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D.,
Giovannoni,J.J. and Martin,G.B.
TITLE Generation of ESTs from Pseudomonas resistant tomato
JOURNAL Unpublished (1999)
COMMENT Contact: CUGI
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES
source
1..456
/organism="Lycopersicon esculentum"
/cultivar="R11-12 (35S::Pto in Rio Grande x Money Maker)"
/db_xref="taxon:4081"
/clone="cLER18J18"
/clone_lib="tomato resistant, Cornell"
/tissue_type="leaf"
/dev_stage="4-week old"
/lab_host="SOLR"
/notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI - Tomato Pseudomonas Resistant EST Library_
Directionally cloned cDNAs inserted into pBluescript SK(-)
at 5' end with EcoRI and 3' end with XhoI site."
BASE COUNT 103 a 114 c 102 g 137 t
ORIGIN
Query Match 42.3%; Score 437.8; DB 9; Length 456;
Best Local Similarity 99.3%; Pred. No. 1.5e-101;
Matches 450; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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QY 19 CTACGTTGAGATAAATATCCCTTTCCTCATTTTCAGTTCCAAAACTCGAAGAGAGA 78
DB 4 CTACGTTGAGATAAATATCCCTTTCCTCATTTTCAGTTCCAAAACTCGAAGAGAGA 63
QY 79 AGAGAACAAATGAAAGGTTTTCACATCGTTTCTTCGACTCGCAATCTGCCTCTCGCAACCGCT 138
DB 64 AGAGAACAAATGAAAGGTTTTCACATCGTTTCTTCGACTCGCAATCTGCCTCTCGCAACCGCT 123
QY 139 GAGTTATGATTTCTCTCAAAAATCTCCGCGAGATCTCACCTCTCGTTCAAACTCATCTCA 198
DB 124 GAGTTATGATTTCTCTCAAAAATCTCCGCGAGATCTCACCTCTCGTTCAAACTCATCTCA 183
QY 199 AGCAGGTGTACCTTACGCTATGCTGTGCTTTAGTGGCATCGGCTGCTGGGCTTACCTTC 258
DB 184 AGCAGGTGTACCTTACGCTATGCTGTGCTTTAGTGGCATCGGCTGCTGGGCTTACCTTC 243
QY 259 ACATTTATGGAATATCGTGGCTCTCTCAACAATGGCTTGCATGGGAAGCATGTGT 318
DB 244 ACATTTATGGAATATCGTGGCTCTCTCAACAATGGCTTGCATGGGAAGCATGTGT 303
QY 319 GGCTTCTCTCAGCTCTCTCTTATCAAGAGCAAAAAGGCTGCTCTTCTGATGGCAGCTG 378
DB 304 GGCTTCTCTCAGCTCTCTCTTATCAAGAGCAAAAAGGCTGCTCTTCTGATGGCAGCTG 363
QY 379 CACTTTTGAAGGCG-CTCTATTTGGTCTCTGATGAGCTGGGCATTAACCTCGATCCA 437
DB 364 CACTTTTGAAGGCGCTCTATTTGCTCTGATGAGCTGGGCATTAACCTCGATCCA 423
QY 438 AGCATTTGTTTGGCGCTTTTGTAGTGTGCT 470
DB 424 AGCATTTGTTTGGCGCTTCTGTAGTGTGCT 456

RESULT 14
AW399750 448 bp mRNA linear EST 18-MAY-2001
LOCUS EST310250 L. pennellii trichome, Cornell University Lycopersicon
DEFINITION pennellii cDNA clone cJPT8N10.5, mRNA sequence.
ACCESSION AW399750
VERSION AW399750.1 GI:6918220
KEYWORDS EST.
SOURCE Lycopersicon pennellii.
ORGANISM Lycopersicon pennellii.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 448)
AUTHORS Alcala,J., Vrebalov,J., White,R., Matern,A.L., Lakey,J., Holt,I.E.,
Liang,F., Hansen,T.S., Upton,J., Ronning,C.M., Craven,M.B., Fujii
C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin
G.B., Tanksley,S.D. and Giovannoni,J.
TITLE Generation of ESTs from wild tomato (Lycopersicon pennellii)
trichomes
JOURNAL Unpublished (1999)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
FEATURES
source
1..448
/organism="Lycopersicon pennellii"
/db_xref="taxon:28526"
/clone="cJPT8N10"
/clone_lib="L. pennellii trichome, Cornell University"
/tissue_type="trichome"
/dev_stage="mixed stages"
/lab_host="SOLR"
/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; Leaves of various stages were shaken in liquid

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nitrogen, shearing off trichomes. This procedure yielded a mixture of cells highly enriched for trichomes, with minor contamination by other types of leaf cells."

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BASE COUNT      107 a   112 c   98 g   131 t
ORIGIN

Query Match      40.9%; Score 423; DB 10; Length 448;
Best Local Similarity 96.6%; Pred. No. 9.3e-98;
Matches 432; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 10 TAACATTGCTACGTTTCAGATAAATATCTTTGCTTCATTTTCAGTTCCAAAACCTCGAAGA 69
Db 2 TATTATTGCTACGTTTCAGATAAATATCTTTGCTTCATTTTCAGTTCCAAAACCTCGAAGA 61
QY 70 AGAAGAAGAGAGACAATGGAAGTTTCACATGTTCTTCGACTCGCAATCTGCCTCTC 129
Db 62 AGAAGAAGAGAGACAATGGAAGTTTCACATGTTCTTCGACTCGCAATCTGCCTCTC 121
QY 130 GCAACCGCTGGAGTTATGATTTCTCTCAAAAACCTTCGGCGAGATCTCACTCTCTGTTCAAA 189
Db 122 GCAACCGCTGGAGTTATGATTTCTCTCAAAAACCTTCGGCGAGATCTCACTCTCTGTTCAAA 181
QY 190 CTCATCTCAAGCAGGTGACCTTAGCTATGCTGTGCTTTAGTGGCATCGGCTGCTGGGG 249
Db 182 CTCATCTCAAGCAGGTGACCTTAGCTATGCTGTGCTTTAGTGGCATCGGCTGCTGGGG 241
QY 250 CTTACCTTCACATTTCTATGGAATATCGGTGGCTCTCTCAACAATGGCTTGCATGGAA 309
Db 242 CTTACCTTCACATTTCTATGGAATATCGGTGGCTCTCTCAACAATGGCTTGCATGGAA 301
QY 310 GCATGCTGGCTTCTCTCAGCTCTCTCTTATPCAGAGCAAAAAGGGTGGCTCTTCTGA 369
Db 302 GCATGATGAGGCTTCTCTCAACTCTCTCTTATPCAGAGCAAAAAGGGTGGCTCTTCTGA 361
QY 370 TGGCAGCTGCACCTTTTGAAGCGCTCTATTTGGTCTCTGATTCAGCTGGGCATTAACT 429
Db 362 TGGCAGCTGCACCTTTTGAAGCGCTCTATTTGGTCTCTGATTCAGCTGGGTATTAACT 421
QY 430 TCGATCCAAAGCATTGTTTGGCGTT 456
Db 422 GCGATCCAAAGCATTGTTTGGCGTT 448

RESULT 15
BE919556      488 bp      mRNA      linear      EST 02-OCT-2000
LOCUS        EST423325 potato leaves and petioles Solanum tuberosum cDNA clone
DEFINITION   cSTB1D22 5' sequence, mRNA sequence.
ACCESSION   BE919556
VERSION     BE919556
KEYWORDS    EST.
SOURCE      potato.
ORGANISM    Solanum tuberosum
REFERENCE   1 (bases 1 to 488)
AUTHORS    van der Hoeven, R.S., Bezzerides, J., Holt, I.E., Liang, F., Cho, J.,
            Utterback, T., Hansen, C.L., Doan, B., Bougri, O., Buell, C.R., Ronning,
            , C.M., Fry, W.E., Tanksley, S.D. and Baker, B.
            Generation of ESTs from potato leaves and petioles
            Unpublished (2000)
TITLE       The Institute for Genomic Research
COMMENT     For clone request, please contact Research Genetics, Libraries
            Division tel 1-800-711-6195, email cdna@resgen.com.
FEATURES
source      1. .488
            /organism="Solanum tuberosum"
            /cultivar="Kennebec"
            /db_xref="taxon:4113"
            /clone="cSTB1D22"
            /clone_lib="potato leaves and petioles"

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/tissue_type="leaflets and petioles"
/dev_stage="8 weeks old plants"
/lab_host="SOLR"

/note="Vector: pBlueScript SK(-); Site 1: EcoRI; Site 2:
XhoI; Tissue was supplied by Dr. Fry (Cornell University).
Leaflets and petioles were isolated from 8 week old
greenhouse grown plants. The plants were watered and
fertilized freely. The tissue was immediately frozen in
liquid nitrogen."

BASE COUNT 110 a 113 c 116 g 149 t
ORIGIN

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Query Match      40.8%; Score 422; DB 12; Length 488;
Best Local Similarity 94.1%; Pred. No. 1.7e-97;
Matches 450; Conservative 0; Mismatches 25; Indels 3; Gaps 1;

QY 6 AACATACATTGCTACGTTTCAGATAAATATCTTTGCTTCATTTTCAGTTCCAAAACCTG 65
Db 14 AAGCAAAACATTGTTAGCTTTAGATAAATAGCCTGTGCTCGTTTCAGTTCCAAAACCTG 72
QY 66 AAGAAGAGAGAGAGACAATGGAAGTTTCACATCGTTCTTCGACTCGCAATCTGCT 125
Db 73 --GAAGAAGAGAGAGAGATAATGAGGGTTTCACATCGTTCTTCGACTCGCAATCTGCT 130
QY 126 TCTCGCAACCGCTGGAGTTATGATTTCTCTCAAAAACCTTCGCGAGATCTCACTCTCGTT 185
Db 131 TCTCGCAACCGCTGGAGTTATGATTTCTCTCAAGAATCTCGCCAGATCTCACTCTCGTT 190
QY 186 CAATCTCATCTCAAGCAGGTGTTACCTTACGCTATGCTGTGCTTTAGTGGCATCGGCTGCT 245
Db 191 CAATCTCATCTCAAGCAGGTGTTACCTTACGCTATGCTGTGCTTTAGTGGCATCGGCTGCT 250
QY 246 GGGGCTTACCTTCACATTCATGGAATATCGGTGGCTCTCTCAACAATGGCTTGCATG 305
Db 251 GGAGCTTACCTTCACATTCATGGAATATCGGTGGCTCTCTCAACAATGGCTTGCATG 310
QY 306 GGAAGCATGCTGGCTTCTCTCAGCTCTCTTATCAAGAGCAAAAAGGGTGGCTCTT 365
Db 311 GGAAGCATGCTGGCTTCTCTCAGCTCTCTTATCAAGAGCAAAAAGGGTGGCTCTT 370
QY 366 CTGATGGCAGCTGCACCTTTTGAAGCGCTCTATTTGGTCTCTGATTCAGCTGGGCATT 425
Db 371 CTGATGGCAGCTGCACCTTTTGAAGCGCTTCTATTGCTCTCTGATTCAGCTGGGCATT 430
QY 426 AACTTCGATCCAAAGCATTGTTTGGCGCTTTTGTAGTTGCTGTGTTTGGTT 483
Db 431 AACTTCGATCCAAAGCATTGTTTGGCGCTTTTGTAGTTGCTGTGTTTGGTT 488

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Search completed: May 25, 2003, 11:25:15
Job time : 1494 secs

GenCore version 5.1.5
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2003, 11:25:24 ; Search time 62 Seconds
(without alignments)
533.002 Million cell updates/sec

Title: US-09-955-526-4

Perfect score: 1272
Sequence: 1 MEGFTSFDDQSASNRWSY.....LIIMLNKASEKKBKKRRN 248

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	688.5	54.1	213	AA365755	Testis Enhanced Ge
2	499.5	39.3	140	AA657556	Testis Enhanced Ge
3	498.5	39.2	138	AA619970	Arabidopsis thalia
4	498.5	39.2	154	AA619969	Arabidopsis thalia
5	495	38.9	110	AA619971	Arabidopsis thalia
6	492.5	38.7	129	AA654829	Bovine mammary tis
7	491.5	38.6	236	AA687615	Arabidopsis thalia
8	483.5	38.0	255	AA658178	Lung cancer assoc
9	477.5	37.5	237	AA673136	Bax inhibitor BI-1
10	331.5	26.1	245	ABP42996	Human ovarian anti

11	324	25.5	277	22	AAU30218	Novel human secret
12	312	24.5	245	22	AB63069	Drosophila melanog
13	192	15.1	305	22	AB57985	Drosophila melanog
14	172	13.5	341	22	AB58798	Drosophila melanog
15	166	13.4	346	21	AA549311	Mouse brown adipos
16	166	13.1	122	21	AA603753	Human secreted pro
17	165	13.0	242	22	AA64490	Human secreted pro
18	165	13.0	345	20	AAW81998	Human adult testis
19	165	13.0	345	21	AAV79139	Human haemopoietic
20	165	13.0	345	21	AAV66631	Membrane-bound pro
21	165	13.0	345	21	AAV59435	Human DERP2 protei
22	165	13.0	345	22	AA65154	Human PRO281 (UNO2
23	165	13.0	345	23	ABP61812	Human polypeptide
24	165	13.0	345	23	ABG34030	Human Pro peptide
25	165	13.0	345	23	AB89838	Human polypeptide
26	165	13.0	346	19	AAW74901	Human secreted pro
27	165	13.0	351	20	AAV76620	Human ovarian tumo
28	165	13.0	351	21	AA643975	Human cancer assoc
29	143.5	11.3	250	22	AA64489	Gene 16 human secr
30	132	10.4	319	21	AA53283	Human TPAAAG12 pol
31	128.5	10.1	241	20	AAV37315	Protein which is s
32	123	9.7	290	21	AA633365	Zea mays protein f
33	123	9.7	324	22	AB60180	Drosophila melanog
34	118.5	9.3	221	21	AA633367	Zea mays protein f
35	118.5	9.3	239	22	AB60197	Drosophila melanog
36	118.5	9.3	243	21	AA633366	Zea mays protein f
37	112.5	8.8	222	21	AA644724	Zea mays protein f
38	112.5	8.8	238	20	AAV59658	Secreted protein f
39	112.5	8.8	250	21	AA644723	Zea mays protein f
40	112	8.8	230	21	AA652201	Arabidopsis thalia
41	112	8.8	245	21	AA652200	Arabidopsis thalia
42	112	8.8	256	21	AA652199	Arabidopsis thalia
43	111	8.7	238	21	AAV77122	Human neurotransm
44	111	8.7	238	22	AA63503	Human polypeptide
45	111	8.7	293	21	AA642202	Human ORFX ORF1966

ALIGNMENTS

RESULT 1
AA65755
ID AA65755 standard; Protein; 213 AA.
XX
AC AA65755;
XX
AC
XX
DT 27-MAR-2001 (first entry)
XX
DE Testis Enhanced Gene Transcript protein #1.
XX
KW Cell death modulator; programmed cell death; PCD; apoptosis;
XX
KW forestry plant.
XX
OS Pinus radiata.
XX
PN WO200075331-A1.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-NZ00086.
XX
PR 04-JUN-1999; 99US-0325932.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
PI Flinn B, Lasham A;
XX
XX WPI; 2001-061724/07.
DR N-PSDB; AAF4782.
XX
XX Novel defender against cell death polynucleotide useful for modulating
PT programmed cell death pathway and specific development pathways in

PT forestry plant -
XX Claim 22; Pages 81-82; 142pp; English.
XX The present invention relates to coding sequences (see AAF44740-F44840
CC and AAF44843-F44844) and proteins (see AAB65714-B65814) involved in
CC programmed cell death (PCD; apoptosis). The coding sequences and proteins
CC of the present invention are useful for modulating a PCD or cell death
CC pathway and various developmental pathways in a forestry plant, by
CC stably incorporating one of the present coding sequences into the genome
CC of the forestry plant, where the coding sequence provides a PCD pathway
CC that is not present in a native form of the forestry plant.
XX SQ Sequence 213 AA;
Query Match 54.1%; Score 688.5; DB 22; Length 213;
Best Local Similarity 64.6%; Pred. No. 3.8e-73;
Matches 137; Conservative 31; Mismatches 41; Indels 3; Gaps 2;
OY 39 QVYLTCCALVASAGAYHILWNGIGLLTTMACGSMVWLLSAP--PYQOKRVALIMA 96
DB 1 RYVLSLSCALVTAAGVYLUHLNLNIGLLTGLACIGSVIGLLSVPTSSNNGKRAALLA 60
OY 97 AALFEGASGPIELGINDPDSIVFGAFVGCVAVFCFSAAAMLARREYLYLGGLLSSG 156
DB 61 AAFKATGATGLIDAVINIDSSILVSFAVGTSLAFACFSAAAITARREYLYLGGLLSG 120
OY 157 VSLFLWLFHFIASSIFGSMVAFKELYFGLLVFVGVIVDTQELIEKALHGMVYKHALT 216
DB 121 ISTIMWLQASSIFGSSAIYFETIYFGLLVFLGVIIFDTQMIIEKADHGVDYKXSLD 180
OY 217 LFTDFGAVFVRILILMKNA-SEKSEKKKKRR 247
DB 181 LFDIDFVAVFRLNVINAKNADSKSREGKKRR 212
RESULT 2
AAB65756
ID AAB65756 standard; Protein; 140 AA.
AC AAB65756;
XX 27-MAR-2001 (first entry)
DE Testis Enhanced Gene Transcript protein #2.
XX Cell death modulator; programmed cell death; PCD; apoptosis;
KW forestry plant.
XX Pinus radiata.
OS WO200075331-A1.
XX 14-DEC-2000.
XX 02-JUN-2000; 2000WO-NZ00086.
XX 04-JUN-1999; 99US-0325932.
XX (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX Flinn B, Lasham A;
XX WPI; 2001-061724/07.
DR N-PSDB; AAF44783.
XX Novel defender against cell death polynucleotide useful for modulating
PT programmed cell death pathway and specific development pathways in
PT forestry plant -
XX Claim 22; Page 82; 142pp; English.

CC The present invention relates to coding sequences (see AAF44740-F44840
CC and AAF44843-F44844) and proteins (see AAB65714-B65814) involved in
CC programmed cell death (PCD; apoptosis). The coding sequences and proteins
CC of the present invention are useful for modulating a PCD or cell death
CC pathway and various developmental pathways in a forestry plant, by
CC stably incorporating one of the present coding sequences into the genome
CC of the forestry plant, where the coding sequence provides a PCD pathway
CC that is not present in a native form of the forestry plant.
XX SQ Sequence 140 AA;
Query Match 39.3%; Score 499.5; DB 22; Length 140;
Best Local Similarity 66.2%; Pred. No. 5.8e-51;
Matches 100; Conservative 14; Mismatches 26; Indels 11; Gaps 2;
OY 1 MEGTSPFDSOSARNRWSYDSLKNFRQISPLVOTHLKQVYLTCCALVASAGAYHIL 60
DB 1 MDAFASLFQS---SGKGMSHDSLKNFRQISPAVQSHLKNYLSLCCALMASAGGAYLHLM 57
OY 61 WNIGGLTTMACGSMVWLLSAPPYQOKRVALIMAALFEGASIGFLIELGINFDPDSIV 120
DB 58 LNIGGLTTIACISIVWLLSIPPHQKQKFGLLMAALFEGACIGFLIELNAIKVDPDSIV 117
OY 121 FOAFVGCVAVFCFSAAAMLARREYLYLGG 151
DB 118 ISAFVGSALAPACFSGAA-----CWLG 140
RESULT 3
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ID AAG19970 standard; Protein; 138 AA.
AC AAG19970;
XX 17-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 21975.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX EP1033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127452.
XX 06-APR-1999; 99US-0128234.
XX 08-APR-1999; 99US-0128714.
XX 16-APR-1999; 99US-0129845.
XX 19-APR-1999; 99US-0130077.
XX 21-APR-1999; 99US-0130449.
XX 23-APR-1999; 99US-0130510.
XX 28-APR-1999; 99US-0130891.
XX 30-APR-1999; 99US-0131449.
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XX 06-MAY-1999; 99US-0132485.
XX 06-MAY-1999; 99US-0132486.
XX 07-MAY-1999; 99US-0132487.
XX 11-MAY-1999; 99US-0132863.
XX 99US-0134256.


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PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
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PR 26-OCT-1999; 99US-0161362.
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PR 28-OCT-1999; 99US-0161393.
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PR 29-OCT-1999; 99US-0162142.

Query Match 39.2%; Score 498.5; DB 21; Length 138;
Best local similarity 70.8%; Pred. No. 7.5e-51;
Matches 91; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QV 1 MEGTSPFDQSASRNWSDSLKNFRQISPLVQTHLKQVYLTCCALVSAAGAYLHL 60
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Db 1 MDAFSSFFDQSGRS-WSYDSLKNFRQISPAVONHLKEVYLTCCALVSAAGAYLHL 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QV 61 WNGGLLTWACMSWYLLSAPPYQOEKEVALLMAALFEFGASIGPLIELGINFDPISIV 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 60 WNGGLITTCIGTMIWLLSCPPYEHQKRLSLTPASVLEGASVGPLIKVAIDVDPISIL 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QV 121 FGAFVGCAY 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 120 ITAFVGTAI 128
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RESULT 4
AAG19969
ID AAG19969 standard; Protein; 154 AA.
XX
AC AAG19969;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 21974.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
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PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
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PR 10-SEP-1999; 99US-0153070.
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PR 16-SEP-1999; 99US-0154039.
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PR 24-SEP-1999; 99US-0155659.
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PR 04-OCT-1999; 99US-0157117.
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PR 21-OCT-1999; 99US-0160815.


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PR 26-OCT-1999; 99US-0161361.
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PR 28-OCT-1999; 99US-0161993.
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PR 28-OCT-1999; 99US-0162142.

Query Match 38.9%; Score 495; DB 21; Length 110;
Best Local Similarity 86.4%; Pred. NO. 1.4e-50;
Matches 95; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 139 MLARREYVLGGLLSSGVSLFLWHPASSIFGGSMAVFKFELYFGLLVFGVYVFDTQE 198
Db 1 MLARREYVLGGLLSSGSLSLWMLQPASSIFGGSASIFKELYFGLLVFGVYVFDTQE 60
QY 199 IIEKAHLGDMYVYKHALTLFTDFGAVFVRILIIIMLNASEKEKKKKRN 248
Db 61 IIEKAHLGDMYVYKHSLLTFTDFVAVFVRILIIIMLNKSADEKKKKRN 110

RESULT 6
AAG54829
ID AAG54829 standard; Protein; 129 AA.
XX AC AAG54829;
XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 70059.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX PR 25-FEB-1999; 99US-0121825.
XX PR 05-MAR-1999; 99US-0123180.
XX PR 09-MAR-1999; 99US-0123548.
XX PR 23-MAR-1999; 99US-0125788.
XX PR 25-MAR-1999; 99US-0126264.
XX PR 29-MAR-1999; 99US-0126785.
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XX PR 06-APR-1999; 99US-0128234.
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XX PR 30-APR-1999; 99US-0132407.
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Query Match 38.7%; Score 492.5; DB 21; Length 129;
Best Local Similarity 71.4%; Pred. NO. 3.5e-50;
Matches 90; Conservative 20; Mismatches 15; Indels 1; Gaps 1;
QY 1 MEGTTFSDQSASRNRSYDLSLKNPQISPLVQTHLKQVYLTCCALVASAAGAYLHL 60
Db 1 MDAFSFFDSQPGSRS-WSYDLSLKNPQISPAVQNHKRVYLTCCALVASAFGAYLHL 59
QY 61 WNTGGLTTMACMGSMWLLSAPPYQEQKRVALLMAALFEGASIGPLIELGINDPSIV 120
Db 60 WNTGGLTTGCTGCTWLLSCPPYEHQKRLSLFASAVLEGASVGLIKVAIDVDP SIL 119
QY 121 FGAFTVG 126
Db 120 ITAFVG 125
RESULT 7
AAB87615
ID AAB87615 standard; protein; 236 AA.
XX AAB87615;
AC AAB87615;
XX AAB87615;
DT 15-MAY-2001 (first entry)
DE Bovine mammary tissue derived protein #6.
XX Bovine; mammary gland; cancer; tumour; angiogenesis.
KW Bos taurus.
OS WO200114553-A1.
XX WO200114553-A1.
PN 01-MAR-2001.
PD 23-AUG-2000; 2000WO-NZ00166.
XX 23-AUG-1999; 99US-0150330.
XX (GENE-) GENESIS RES & DEV CORP LTD.
PA (NZPA-) NEW ZEALAND PASTORAL AGRIC RES INST LTD.
XX Havukkala IJ, Gleen M, Grigor MR, Molenaar AJ;
PI WPI; 2001-226619/23.
XX New polypeptides and polynucleotides encoding the polypeptides, which
PT are expressed in bovine mammary gland tissue, useful for stimulating
PT mammary gland growth or function, or inducing differentiation of milk
PT producing cells -
XX Claim 11; Page 62; 97pp; English.
PS The present invention relates to proteins derived from bovine
XX mammary gland cells. The invention is useful for stimulating
CC bovine mammary gland cell growth and function, inhibiting the
CC growth of various mammary gland cancer cells, inhibiting
CC angiogenesis and vascularization of tumours, or modulating
CC the growth of blood vessels in a mammal.
XX Sequence 236 AA;
SQ

Query Match 38.6%; Score 491.5; DB 22; Length 236;
Best Local Similarity 42.9%; Pred. No. 1e-49;
Matches 99; Conservative 53; Mismatches 72; Indels 7; Gaps 4;

QY 19 SYDSLKNFROISPLVQTHLKVYTLCCALVASAAGAYLHILWNI--GGLLTMACGSM 76
Db 9 NFDALFRFSHITSTQOHLKKVYASALCMFVAAGAYIHVVTHFIQAGLLSALGSLGM 68
QY 77 VWLTSAPPYQ--EQRKVALMAAALFEGASIGLELGINFDPFSIVFGACAVVFCF 134
Db 69 IWLWATPHSHETEQRKGLLAGFAFLTGVLGPAALDCAINPSILPTAFMGTAIFTCF 128
QY 135 SAAMLAARREYILVGLLSSGVSLFWLHFASISFGGSMAYEKPELVGLAVFVGYIVE 194
Db 129 TLSALYARRRSYFLGGLILMSALML--LSSLGNIFFGSVWLFQANLYMGLVVMCGFVLF 187
QY 195 DTQRIIEKAHLGDMYVYKHALTFTDFGAVFVRILIMLKNASEKEEKKK 245
Db 188 DTQLIIEKAENGDKYIWHCVDFLDFVTLFRKLMMILAWN--EKDKKKK 236

RESULT 8
AAB58178
ID AAB58178 standard; Protein; 255 AA.
XX AC AAB58178;
XX DT 14-MAR-2001 (first entry)
XX DE Lung cancer associated polypeptide sequence SEQ ID 516.
XX KW Human; lung cancer associated protein; neuroprotective; cytostatic;
KW KMO cardioactive; immunomodulatory; muscular active; vulnerary;
KW KMO gastrointestinal; nephrotropic; antiinfective; gynecological;
KW KMO antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
KW KMO proliferative disorder; wound healing; infectious disease.
XX OS Homo sapiens.
XX PN W0200055180-A2.
XX PD 21-SEP-2000.
XX PF 08-MAR-2000; 2000WO-US05918.
XX PR 12-MAR-1999; 99US-0124270.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (ROSE/) ROSEN C.A.
XX FI Ruben SM;
XX DR WPI; 2000-587514/55.
XX DR N-PSDB; AAF18054.
XX PT Lung cancer associated gene sequences, referred to as lung cancer
XX PT antigens, useful for treatment, prevention, and diagnosis of disorders
XX PT such as lung cancer -
XX PS Claim 11; Page 1006-1007; 1425pp; English.
XX CC Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer
CC CC associated proteins represented in AAB58106 - AAB58548. Lung cancer
CC CC associated proteins and polynucleotide sequences, their agonists, and
CC CC antagonists may have neuroprotective; cytostatic; cardioactive;
CC CC immunomodulatory; muscular active general; vulnerary; gastrointestinal
CC CC general; nephrotropic; antiinfective; gynecological; or antibacterial
CC CC activity. The invention also includes antibodies specific for the
CC CC protein or polynucleotide sequences. The lung cancer associated
CC CC polynucleotide sequences may be used for detection of lung cancer,
CC CC chromosome identification, as chromosome markers, and for numerous other
CC CC diagnostic or research purposes. The proteins may be used to treat
CC CC disorders such as neural, immune, muscular, reproductive,

CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders. The proteins may also be used in the treatment of wounds and
CC infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and
CC peptide AAB58549 are used in the course of the invention for the
CC identification and characterisation of the polynucleotide and protein
CC sequences.
XX SQ Sequence 255 AA;
Query Match 38.0%; Score 483.5; DB 21; Length 255;
Best Local Similarity 41.1%; Pred. No. 1e-48;
Matches 102; Conservative 54; Mismatches 79; Indels 13; Gaps 5;

QY 3 GFTSFDSOSASRNKWSYSLKFRQISPLVQTHLKVYTLCCALVASAAGAYLHILWN 62
Db 17 GTWNIIFD-----RKINFDALKFHSHTIPSTQOHLKKVYASALCMFVAAGAYVHVYTH 70
QY 63 I--GGLTTMACGSMVWLLSAPPYQ--EQRKVALMAAALFEGASIGLELGINFDPFS 118
Db 71 FIQAGLLSALGSLILMILWLAIPHSHETEQRKGLLAGFAFLTGVLGPALEFCIAVNPS 130
QY 119 IVFGAFVGCNAVVEGCFSAAMLAARREYILVGLLSSGVSLFWLHFASISFGGSMAYEK 178
Db 131 ILPTAFMGTAIFTCFTLSALYARRRSYFLGGLILMSALSL--LSSLGNIFFGSVWLFQ 189
QY 179 FELYGLLVFVGYIVFDTQRIIEKAHLGDMYVYKHALTFTDFGAVFVRILIMLKNASE 238
Db 190 ANLYVGLVVMCGFVLFDTQLIIEKAENGDDYIWHCIDLDFLDFITVFRKLMMILAWN--E 247
QY 239 KEKKKKR 246
Db 248 KDKKKKK 255

RESULT 9
AAW73136
ID AAW73136 standard; Protein; 237 AA.
XX AC AAW73136;
XX DT 02-FEB-1999 (first entry)
XX DE Bax inhibitor BI-1.
XX KW Bax inhibitor; BI-1; human; apoptosis.
XX OS Homo sapiens.
XX PH Key Location/Qualifiers
XX FT Domain 30..50 /note= "transmembrane domain"
XX FT Domain 55..73 /note= "transmembrane domain"
XX FT Domain 85..103 /note= "transmembrane domain"
XX FT Domain 117..135 /note= "transmembrane domain"
XX FT Domain 141..160 /note= "transmembrane domain"
XX FT Domain 162..187 /note= "transmembrane domain"
XX PN W09840397-A1.
XX PD 17-SEP-1998.
XX PF 13-MAR-1998; 98WO-US05015.
XX PR 14-MAR-1997; 97US-0818514.
XX PA (BURN-) BURNHAM INST.
XX PI Reed JC, Xu Q;

XX WPI; 1998-531519/45.
DR N-PSDB; AAV59067.
XX Bax inhibitor proteins, Bi-1 and Bi-2 - useful e.g. to modulate
PT cellular apoptotic activity or identify agents altering Bi-1 or Bi-2
PT binding which can modulate apoptotic activity
XX
XX Claim 14; Fig 1; 80pp; English.
XX
XX This is the amino acid sequence of an inhibitor protein, termed .
CC Bi-1, of the pro-apoptotic protein Bax. Nucleic acids encoding
CC Bi-1 (see AAV59067) and Bi-2 (see AAV59068) were identified by
CC suppression of Bax-induced death of yeast cells transformed to
CC express human Bax. A human HepG2 cDNA library was used for library
CC screening. The invention provides vectors, optionally expression
CC or viral vectors, containing Bi nucleic acids, and host cells
CC containing these vectors.
CC be used to increase expression of these proteins in cells, or
CC antisense molecules prepared from them used to decrease expression.
CC In these ways, cellular apoptotic activity may be modulated. The
CC Bis and peptide portions are useful to detect, e.g. another Bi or a
CC member of the Bcl-2 family in biological samples. They are
CC especially useful in assays to identify agents (e.g. organic
CC molecules or peptides; claimed) modulating the specific association
CC of Bi-1/Bi-2 with a second protein (e.g. a Bi, an anti-Bi antibody
CC or a Bcl-2 family protein (e.g. Bax) (Claimed)) e.g. in screening
CC for drugs to treat pathologies characterised by aberrant apoptotic
CC activity. The agents can then be contacted with cells to modulate
CC cellular apoptotic activity (claimed). Bax overexpression is
CC associated with e.g. neuronal cell death due to ischaemia, epilepsy,
CC spinal cord injury, Parkinson's disease and Alzheimer's disease.
CC Antibodies raised against the Bis and peptides are also useful e.g.
CC to detect/quantify Bis in biological samples.
XX Sequence 237 AA;
SQ
Query Match 37.5%; Score 477.5; DB 19; Length 237;
Best Local Similarity 42.2%; Pred. No. 4.8e-48;
Matches 98; Conservative 53; Mismatches 74; Indels 7; Gaps 4;
QY 19 SYDSLKNFRQISPLVQTHLKQVYLTCCALVASAAGAYHLHWN1--GGLTTMACWGS 76
DB 9 NFDALLKFHSHTPTQCHLKVKYASFPALCMFVAARAGAYVHMVTHFIOAGLLSALGSLIM 68
QY 77 VWLLSAPPVQ--EOKRVALLMAALFEGASIGLTELGNFDPSPVFCGAVGCAVFGCF 134
DB 69 IWLMPHSHETEQKLGKLLAGFAFLTGGLGPALEFCIAVNPSSLPTAFMGTAIVTCTP 128
QY 135 SAAMLARREYLYLGGLLSSGVSLLFWLHFASSIFGGSMVAFKFLYFGLLVFGYIVF 194
DB 129 TSLGALYARRRSYFLGGILMSALSILL--LSSLGNVFFGSIWLFQANLVGLVWCGFVLF 187
QY 195 DTQETIEKAHLGMDYVKHALTFDTFGAVFVRILLIMLKNASEKKEKKR 246
DB 188 DTQLIIEKAEBGQDYVHCIDFLDFITVFRKLMMILANN--EKDKKKKK 237
RESULT 10
ABP42996
ID ABP42996 standard; Protein; 245 AA.
XX
XX ABP42996;
AC
XX
XX 22-AUG-2002 (first entry)
DT
XX Human ovarian antigen HPDWT56, SEQ ID NO:4128.
DE
XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW

cardiovascular disorder; respiratory disorder; neurological disorder;
gastrointestinal disorder; urinary system disorder; drug screening;
gene therapy; chromosome mapping; forensic analysis;
antibody preparation; cytostatic; immunomodulatory; neuroprotective;
antiinflammatory; gynaecological; reproductive.
Homo sapiens.
WO200200677-A1.
XX
XX 03-JAN-2002.
XX
XX 07-JUN-2001; 2001WO-US18569.
XX
XX 07-JUN-2000; 2000US-209467P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Birse CE, Rosen CA;
PI
XX WPI; 2002-147878/19.
DR N-PSDB; ABQ56073.
XX
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT useful in the prevention, treatment and diagnosis of cancer (e.g.
PT ovarian cancer), immune disorders, cardiovascular disorders and
PT neurological diseases -
XX
XX Claim 11; SEQ ID NO 4128; 2922pp; English.
XX
XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 245 AA;
SQ
Query Match 26.1%; Score 331.5; DB 23; Length 245;
Best Local Similarity 34.8%; Pred. No. 1.1e-30;
Matches 72; Conservative 46; Mismatches 78; Indels 11; Gaps 4;
QY 3 GFTSPFDQSASRNWSYDSLKNFRQISPLVQTHLKQVYLTCCALVASAAGAYHLHWN 62
DB 17 GTWNIFD-----RKINFALLKFHSHTPTQCHLKVKYASFPALCMFVAARAGAYVHMVTH 70
QY 63 I--GGLTTMACWGSWVLLSAPPVQ--EOKRVALLMAALFEGASIGLTELGNFDPSP 118
DB 71 FIOAGLLSALGSLIMVLMATPHSHETEQKLGKLLAGFAFLTGGLGPALEFCIAVNP 130

QY 119 IVFGAFVGCVAVFGCSAAAMLARREYLYLGGLLSSGVSLLPWLHFASSIFGGSMVAFK 178
 Db 131 ILPFAFWGTAMIFCTLSALYARRSYLFLGGLMSSPELGAFASLNGFPF-GSINLFPQ 189
 QY 179 FELYGLLVFVGVYVFDTOEIIKAHL 205
 Db 190 ANLYXGLVVMCGPFAFLINLSLLKRPNM 216

RESULT 11

AAU30218
 ID AAU30218 standard; Protein; 277 AA.

AC AAU30218;

DT 18-DEC-2001 (first entry)

DE Novel human secreted protein #709.

XX Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

OS Homo sapiens.

XX WO200179449-A2.

FN 25-OCT-2001.

XX 16-APR-2001; 2001WO-US08656.

XX 18-APR-2000; 2000US-0552929.

PR 26-JAN-2001; 2001US-0770160.

XX (HYSE-) HYSEQ INC.

FA Tang YT, Liu C, Drmanac RT;
 PI WPI; 2001-611725/70.

XX Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -

XX Claim 20; Page 262; 765pp; English.

PS The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.

XX Sequence 277 AA;

Query Match 25.5%; Score 324; DB 22; Length 277;

Best Local Similarity 35.0%; Pred. No. 9.8e-30;

Matches 93; Conservative 51; Mismatches 88; Indels 34; Gaps 13;

QY 3 GFTSPDOSASRNWSYDSLKNFQISPLV-QTHLKVYITLCCALVSAAGAYHLHM 61

Db 17 GTMNIPD-----RKITFDALLKFHSITFSTQQAHRMKKVASFALCYFGAAGAYVNMVT 70

QY 62 NI--GGILTTMACMGSMVWLLGAPPYQ--EOKRV--ALIMAAALFEGASIGPLI---ELG 112
 Db 71 HFTQAGLLSALGSLILMIWLMATPHSHETEQLKGTSLGFCIPYRKLGLGALGSFVIA 130
 QY 113 INFDPISIVFOAFVGC-A-VVFGCSAAAMLAR-REYLYLGGLLSSGVSL-LFWLHFASSI 169
 Db 131 VKRQASLP-TAFMGHSGNSFPAPTLSALLCRPRSYLFLGGILMSALSIVAFCLPLGNVF 189
 QY 170 FGGSMVAFKPELYGLLVFVGVYVFDTOEIIKAHLGDMDY-VKHALTLFTDFGAVFVRI 228
 Db 190 FWIPFVVFQANLYVGLVVMCGFVLFDTQLIIKABQGDQDYNLWHCIDLFLDFITVF--- 246
 QY 229 LIIMLNASE-----KEEKKKKRRN 248
 Db 247 ----QKNSMKDPGPFMKKDKKKRRN 268

RESULT 12

ABB63069

ID ABB63069 standard; Protein; 245 AA.

AC ABB63069;

XX 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 15999.

XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.

XX Drosophila melanogaster.

FN WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

XX N-PSDB; ABL07172.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -

XX Disclosure; SEQ ID NO 15999; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABLL16176-ABLL30511), expressed DNA
 CC sequences (ABLL1840-ABLL16175) and the encoded proteins
 CC (ABBS7737-ABBS72072).

XX The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 245 AA;

Query Match 24.5%; Score 312; DB 22; Length 245;

Best Local Similarity 34.4%; Pred. No. 2.2e-28;

Matches 77; Conservative 48; Mismatches 83; Indels 16; Gaps 5;

QY 31 PLVOTHLKQVYLTCCALVSAAGAYLHI--LWNIGLLTTMACGSMWVLLSAPPYQEQ 88
 Db 25 PVREHLKQVYVWLGSTAAATANGMLQMRDFLDG---VLAATVILVVLGLHYKDD 80
 QY 89 -----KRVALLMAALFPGASIGPLIEIGINFDPSIVFGAFVGCNAVFGCFSAAMLARR 143
 Db 81 GKNVYTRLGMLYAFGCSGQTLGPLIGVICSINPAIILSALTGTFTVFSLSLSALLAEQ 140
 QY 144 RYVYLGGLSSGVSLFWLHPASSIFGSMVAFKFLYFGLLVFVGIVYVDFDQIIEKA 203
 Db 141 GKLYLGGMLVSVIMTALLSLFNWVF-KSYFVQVTQYVGVFWMAAFIVDTQNIIVEK 199
 QY 204 HGDMDYVKHATLFTDFGAVFVRILIMLNKASEKEKKRR 247
 Db 200 RGNREVVQHALDFDVLSPFRLLIIL----TKBERKQNER 239

RESULT 13
 ABB57985
 ID ABB57985 standard; Protein; 305 AA.
 AC ABB57985;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 747.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL02088.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Disclosure; SEQ ID NO 747; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB101840-AB130511), expressed DNA
 CC sequences (AB101840-AB116175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 305 AA;
 Query Match 15.1%; Score 192; DB 22; Length 305;
 Best Local Similarity 25.7%; Pred No 5, 2e-14;
 Matches 61; Conservative 49; Mismatches 87; Indels 40; Gaps 8;
 QY 36 HLKQVYLTCCALVSAAGAY-----LHILWNIIGLLTTMACM-----GSMVLLSAPP 84

Db 85 HATYAFGASGVTAASAVAFQSDAMMALMTRSGWVASLVTGLVWLSGSIQAQGLEYP 144
 QY 85 YQEKRVALLMAALFPGASIGPLIEIGINFDPSIVFGAFVGCNAVFGCFSAAMLARR 144
 Db 145 GFQAKQALAWLHVCAVL-GAVLAPWCLLG---GPILTKALLYTSIGVIGALSTVACAPSE 199
 QY 145 EYLYLGGILSSGVSLF-----WLHFASSIFGSMVAFKFLYFGLLVFVGIVYVDFDQ 197
 Db 200 KFLHWGGPLAIGLVGFVASSLASMWLPPTTAVGAG--LASMSLYGGLILFSGFLLYDQ 256
 QY 198 EIEKAHLGDM-----DYVKHALTFTDFGAVFVRILIMLNKASEKEKKRRN 248
 Db 257 RIVKSAELYPQSKFPYDPINHALAYMDALNIFIRAILAGD-----QKRN 305

RESULT 14
 ABB5798
 ID ABB5798 standard; Protein; 341 AA.
 AC ABB5798;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 3186.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL02901.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Disclosure; SEQ ID NO 3186; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
 CC sequences (AB101840-AB116175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 341 AA;
 Query Match 13.5%; Score 172; DB 22; Length 341;
 Best Local Similarity 26.5%; Pred No 1, 4e-11;
 Matches 56; Conservative 46; Mismatches 77; Indels 32; Gaps 9;
 QY 46 CALVASACAYL--HILWNI---GGLLTTMACM-----GSMVLLSAPPYQEKRVALL 94

Search completed: May 25, 2003, 12:20:50
Job time : 64 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	688.5	54.1	213	4	US-09-325-932A-87	Sequence 87, Appl
2	499.5	39.3	140	4	US-09-325-932A-88	Sequence 88, Appl
3	477.5	37.5	237	2	US-08-818-514-3	Sequence 3, Appl
4	477.5	37.5	237	4	US-09-115-934A-3	Sequence 2, Appl
5	165	13.0	346	4	US-09-362-123A-2	Sequence 493, App
6	165	13.0	346	4	US-09-149-476-493	Sequence 89, Appl
7	112.5	8.8	238	4	US-09-247-155-89	Sequence 1, Appl
8	109	8.6	311	2	US-08-794-216-1	Sequence 1, Appl
9	107	8.4	369	2	US-08-749-289-1	Sequence 28, Appl
10	96.5	7.6	237	4	US-09-372-422A-28	Sequence 30, Appl
11	95.5	7.5	249	4	US-09-372-422A-30	Sequence 3, Appl
12	94.5	7.4	516	2	US-08-794-216-3	Sequence 3, Appl
13	94.5	7.4	516	2	US-08-749-289-3	Sequence 26, Appl
14	94	7.4	272	4	US-09-372-422A-26	Sequence 12, Appl
15	87	6.8	607	1	US-07-879-617A-12	Sequence 12, Appl
16	87	6.8	607	1	US-08-753-985-12	Sequence 34, Appl
17	82	6.4	234	4	US-09-372-422A-34	Sequence 7, Appl
18	81	6.4	607	1	US-07-959-943-7	Sequence 9, Appl
19	81	6.4	630	1	US-07-959-943-9	Sequence 2, Appl
20	81	6.4	653	1	US-07-782-298-2	Sequence 10, Appl
21	81	6.4	1711	3	US-08-369-822C-10	Sequence 10, Appl
22	81	6.4	1711	3	US-08-582-776C-10	Sequence 10, Appl
23	81	6.4	1711	3	US-08-334-631B-10	Sequence 10, Appl
24	79.5	6.2	249	4	US-09-372-422A-22	Sequence 22, Appl
25	79.5	6.2	249	4	US-09-372-448A-6	Sequence 46, Appl
26	79.5	6.2	515	2	US-09-073-362-3	Sequence 3, Appl
27	79.5	6.2	515	2	US-09-243-920-3	Sequence 3, Appl


```
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325.932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 88
LENGTH: 140
TYPE: PRT
ORGANISM: Pinus radiata
US-09-325-932A-88

Query Match      39.3%; Score 499.5; DB 4; Length 140;
Best Local Similarity 66.2%; Pred. No. 4.7e-51;
Matches 100; Conservative 14; Mismatches 26; Indels 11; Gaps 2;

QY 1 MEGFTSFDSASNRWSYSLKNFRQISPLVQTHLKQVYLTCCALVSAAGAYLHL 60
DB 1 MDAFASLFQS---SGKWSHSDSLNFRQISPAVQSHLKNVYLSLCCALMASAGAYLHL 57
QY 61 WNIIGLLITTMACGSMYLLSAPPYQKQKVALIMAAALFEGASIGLIELGINFDPSTV 120
DB 58 LNIIGLLITTIACIGSIWLLSIPHEQKQKFGLLMAALFEGACIGLIELAIAIKVDPSIV 117
QY 121 GFAGVCAVFCGSAAMLARREYLYLGG 151
DB 118 ISAFVGSALAFCSGAA-----CWLEG 140

RESULT 3
US-08-818-514-3
; Sequence 3, Application US/08818514
; Patent No. 5837838
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: BAX Inhibitor Proteins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,514
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2446
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-818-514-3

Query Match      37.5%; Score 477.5; DB 2; Length 237;
Best Local Similarity 42.2%; Pred. No. 3.8e-48;
Matches 98; Conservative 53; Mismatches 74; Indels 7; Gaps 4;

QY 19 SYDSLKNFRQISPLVQTHLKQVYLTCCALVSAAGAYLHLWNI--GGLLTTMACGSM 76
DB 9 NFDALLKFSHTPTQQLKKVYSPALCNFVAAGAYVHVTHFIOAGLLSALGSLIIM 68
QY 77 VMLSAPPYQ--EQRVALLMAALFEGASIGLIELGINFDPSTVIFGAFVCAVFGCF 134
DB 69 IWMATPHSHETEOKKLGLAGFAFLTGIGLGPALFECIAVNPISILPTAFMGTAIIFTCF 128
QY 135 SAAAMLARRRYLYLGLLSSGVSLFLHFASSIFGGSMAVFKFELYFGLLVFGYIVF 194
DB 129 TILSALYARRRYLYLGLLMSALSLL--LSSLGNVFPFSGIWLFOANLYVGLVVMCGVILF 187
QY 195 DTCEILIEKAHLGMDYVKHALTFTDFGAVFVRLIIMLKNASEKEKKKKR 246
DB 188 DIQLIEKAHGDQDIWHCIDLFDLFDITVFRKLMLAMN--EKDKKKKK 237

RESULT 4
US-09-115-934A-3
; Sequence 3, Application US/09115934A
; Patent No. 6130317
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: BAX Inhibitor Proteins
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/115,934A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/818,514
; FILING DATE: 14-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 3209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-115-934A-3

Query Match      37.5%; Score 477.5; DB 4; Length 237;
Best Local Similarity 42.2%; Pred. No. 3.8e-48;
Matches 98; Conservative 53; Mismatches 74; Indels 7; Gaps 4;

QY 19 SYDSLKNFRQISPLVQTHLKQVYLTCCALVSAAGAYLHLWNI--GGLLTTMACGSM 76
DB 9 NFDALLKFSHTPTQQLKKVYSPALCNFVAAGAYVHVTHFIOAGLLSALGSLIIM 68
QY 77 VMLSAPPYQ--EQRVALLMAALFEGASIGLIELGINFDPSTVIFGAFVCAVFGCF 134
DB 69 IWMATPHSHETEOKKLGLAGFAFLTGIGLGPALFECIAVNPISILPTAFMGTAIIFTCF 128
QY 135 SAAAMLARRRYLYLGLLSSGVSLFLHFASSIFGGSMAVFKFELYFGLLVFGYIVF 194
DB 129 TILSALYARRRYLYLGLLMSALSLL--LSSLGNVFPFSGIWLFOANLYVGLVVMCGVILF 187
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[illegible]

EARLIER APPLICATION NUMBER: 60/056,877
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,889
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,893
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,630
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,878
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,662
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,872
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,882
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,637
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,903
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,888
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,879
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,880
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,894
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,911
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,636
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,874
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,910
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,864
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,631
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,845
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,892
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,599
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,585
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,586
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,589
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670

EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 13.0%; Score 165; DB 4; Length 346;
Best Local Similarity 26.3%; Pred. No. 4.1e-11;
Matches 61; Conservative 47; Mismatches 86; Indels 38; Gaps 11;

QY 36 HUKQVTLCCALVASAAGYLH--ILWNI---GGLT---TWACMGSMVWILSAPPYQE 87
DB 125 HSTMYLAGSISGLTALSALISRTPLMNFMRGSGWTIGTFAAMVAGMLVRSIPYDQ 184
QY 88 Q---KRVALLMAALFEASIGPLIEGINFDPISVFGAFVGCAGVFGCFSAAMLARR 144
DB 185 SPGKHLAWLLHSGVM--CAVAPLTILG---GPLLIRAAVMTAGIV--GGLSTVAMCAPSE 239
QY 145 EYVYLGGLSSGVSLFLWHPASSIFGSGM-----AVKPELYFGLLVFVGIVF 194
DB 240 KFLNMGAPLGVGLGV---FVSSL--GSMPLPTTVAGATLYSVAMYGLVFSMPLLY 293
QY 195 DTQEITEKARLGD-----DYVKHALTLFTDFGAVFVRILIIMLKNASEKE 240
DB 294 DTQVKIKRAEYSPMGVQKYPINSLSIYMDTLNIFRVATMLATGGRKK 345

RESULT 7
US-09-247-155-89
Sequence 89, Application US/09247155A
Patent No. 6312922
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclet, Aymeric
APPLICANT: Bougueret, Lydie
TITLE OF INVENTION: Complementary DNAs
FILE REFERENCE: GENSET.021A
CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/081,563
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER FILING DATE: 1998-08-10
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-10-04

;/ NUMBER OF SEQ ID NOS: 182
;/ SOFTWARE: Patent.pm
;/ SEQ ID NO 89
;/ LENGTH: 238
;/ TYPE: PRT
;/ ORGANISM: Homo sapiens
;/ FEATURE:
;/ NAME/KEY: SIGNAL
;/ LOCATION: -53...-1
US-09-247-155-89

Query Match 8.8%; Score 112.5; DB 4; Length 238;
Best Local Similarity 23.3%; Pred. No. 3.7e-05;
Matches 54; Conservative 36; Mismatches 67; Indels 75; Gaps 11;
QY 50 ASAAGAYLHI-----LWNIGGLTTMACGSMVWLLSAPPYQEKRV-----ALLMA 96
DQ 21 SSVASATVHRAFLKRVVLSLQVLLTTVTSVFL-----YFESVRTFVHSPALL- 74
QY 97 ALFEGASIGPLIELGIN-----FDPISIVGAFVCCA 128
DQ 75 --LFGALSLGLIFALITLRHKYPLNLYLLFGFTLEALTVAWVTFYDVYIILQAFILTT 132
QY 129 VVFGCFSA--MLARRRYLYLGLLSGVSLFWLHPASSIFGSMVAFKFELY----- 182
DQ 133 TVF--FGLTVYTLQSKDFSKFG-----AGLFWLLWILCLSGF-----LKFFLYSEINE 179
QY 183 -----FGLLVFVGVYVFDTOELIEKAHLGDMYVGHALTFTDFGAVFVRIL 229
DQ 180 LVLAAGALLFCGFIYDTHSLMK--LSPEYVLAATSLYLDIINFLHL 229

RESULT 8
US-08-794-216-1
; Sequence 1, Application US/08794216
; Patent No. 5843716
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Coleman, Roger
; TITLE OF INVENTION: NOVEL PROLINE-RICH MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/794,216
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0196 US
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 311 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

;/ TOPOLOGY: linear
;/ IMMEDIATE SOURCE:
;/ LIBRARY: Consensus
;/ CLONE: Consensus
US-08-794-216-1
Query Match 8.8%; Score 109; DB 2; Length 311;
Best Local Similarity 24.6%; Pred. No. 0.00014;
Matches 49; Conservative 28; Mismatches 76; Indels 46; Gaps 9;
QY 41 YLTCCALVASAAGAYLHILWNIGGLTTMACGSMVWLLSAPPYQEKRVALLMAALF 100
DQ 148 YLLIAC-----CQPRRRFPWNILLTLTFANGFTGTGVISS-WYQTK---AVIIAMIT 198
QY 101 EGASIGPLIELGINFDPISIVGAFVGCFAVFGFSAAAMLARREYLYLGLLSGV--- 157
DQ 139 AVWSISVTI---FCQTKVDFTSCTGLFCVLGI-----VLLVTGIVTSIVLYF 243
QY 158 SLLFWLHPASSIFGSMVAFKFELY--FGLLVFVGVYVFDTOELI--EKAHLGDMYVGH 213
DQ 244 QYVWLEM-----LYAALGAICTFLFLAYDTQLVLGNRKHITSPEDYITG 288
QY 214 ALTLFTDFGAVFVRILIM 232
DQ 289 ALQIYTDIIYVTFEVLQLM 307

RESULT 9
US-08-749-289-1
; Sequence 1, Application US/08749289
; Patent No. 5955301
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Coleman, Roger
; TITLE OF INVENTION: NOVEL HUMAN GLUTAMATE-BINDING
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,289
; FILING DATE: Filed Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0160 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: 386116
US-08-749-289-1

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Query Match      8.4%; Score 107; DB 2; Length 369;
Best Local Similarity 20.8%; Pred. No. 0.0003;
Matches 57; Conservative 41; Mismatches 90; Indels 86; Gaps 11;

QY 2 EGTSTFDSQSASRNSWDSLNKFRQISPLVQTHLKQVYLTLCAL-----V 49
DB 134 EGPSYDQDFPATWDDKSIR-----QAFIRKVELVLTQLSVLTSTVSFTFV 184
QY 50 ASAG-----AY-----LHIL-----WNIGLLTTMACGSMWLLS 81
DB 185 AEVGFVRENWVYVYAVFFSLIVLSLSCDGRKHPNVLVALSVLTASISYVGM1- 243
QY 82 APYQOKRVALMAALPEGASIGPLI-ELGINFDPISVFGAFVGCFAVFCFSAAAML 140
DB 244 ASFYNT-----AVIMAGITTAFTVIFSMQTRDYFTSCMGVLVSVVLFIFAILCIP 300
QY 141 ARREVLVYLGILLSSGVSLFVLMHFASSIFGGSMAVFKFELYGLLVFGVYVFDQII 200
DB 301 IRNR-----ILEIVAS-----LGALLFTCFPLAVDTQLL 330
QY 201 --EKALGDMYKHAITLFTDFGAVFVRLIIM 232
DB 331 GNKQLSLPEEYVFAALNLYTDIINFILYLTII 364

RESULT 10
US-09-372-422A-28
; Sequence 26, Application US/09372422A
; Patent No. 6313375
; GENERAL INFORMATION:
; APPLICANT: Rudolf Jung
; TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
; FILE REFERENCE: 0919
; CURRENT APPLICATION NUMBER: US/09/372,422A
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: US 60/098,692
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Zea mays
US-09-372-422A-28

Query Match      7.6%; Score 96.5; DB 4; Length 257;
Best Local Similarity 24.1%; Pred. No. 0.0031;
Matches 40; Conservative 33; Mismatches 58; Indels 35; Gaps 7;

QY 32 LVQTHLKQV--YLTLCALVASAAGAVLHILWNIGLLTTMACGSMWLLSAPPYQEQK 89
DB 99 LVRGHITKRALLYVAAQLASSACIL-LRYLSGGVWTPVHALGAGI-----RPNQGLV 152
QY 90 RVALMAALP-----EGASIGPLIELGINFDPISVFGAFVGC-AVVGCFCSAA 137
DB 153 NEVILTFSLFVTVAMILDPRSQVRTIGPLT-----GLVAGNSLAGGNFTGA 201
QY 138 AMLARRREVLVYLGILLSSGVSLFVLMHFASSIFGGSMAVFKFELYF 183
DB 202 SMNPARS-----FGPAMATGVWTHWVYVIGLIGGSLAGVYSLSF 243

RESULT 11
US-09-372-422A-30
; Sequence 30, Application US/09372422A
; Patent No. 6313375
; GENERAL INFORMATION:
; APPLICANT: Rudolf Jung
; TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
; FILE REFERENCE: 0919
; CURRENT APPLICATION NUMBER: US/09/372,422A
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: US 60/098,692
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Zea mays
US-09-372-422A-30

Query Match      7.5%; Score 95.5; DB 4; Length 249;
Best Local Similarity 25.3%; Pred. No. 0.0039;
Matches 38; Conservative 22; Mismatches 65; Indels 25; Gaps 5;

QY 42 IYLCALVASAAGAVLHILWNIGLLTTMACGSMWLLSAPPYQEQKRVALLMA----- 96
DB 102 LYIAAQLASSAACPL-LRWLTGGLATFVHALAEGVPLQGVVAEAVFTFSLFVIYATI 160
QY 97 ---AALFEGASIGPLIELGINFDPISVFGAFVGCFAVVGCFCSAAAMLARRREVLVYLG 153
DB 161 LDPRKLLPGA--GPLLT-----GLLVGANSVAGAALSGASMPARSF---GPAV 204
QY 154 SSGVSLFVLMHFASSIFGGSMAVFKFELYF 183
DB 205 ASGVWTHWVYVWVGLAGGLAVLVYECCF 234

RESULT 12
US-08-794-216-3
; Sequence 3, Application US/08794216
; Patent No. 5843716
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Coleman, Roger
; TITLE OF INVENTION: NOVEL PROLINE-RICH MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-Seq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/794,216
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0196 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 516 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
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CLONE: 238267
US-08-794-216-3

Query Match 7.4%; Score 94.5; DB 2; Length 516;
Best Local Similarity 21.4%; Pred. No. 0.014;
Matches 56; Conservative 48; Mismatches 95; Indels 63; Gaps 14;
QY 2 EGFSPFDSQASRNRWSYSLKXFRQISPLVQTHLKQVYLTLCAL-VASAAGAYLHL 60
DB 111 EGPSPYDNDQFPNVND-----KSIR-----QAFIRKVFVLTLQSLVTSTVAITFFV 160
QY 61 WNIGGL-----LTTMACGSMWMLLSAPPYQEQKRVALLMAALFEG 102
DB 161 GEVKGFRANWTVYVSAIFFISLIVLSCGDF-----RKHPNWLVALSILT- 209
QY 103 ASIGPLIELGINF--DPSIVFGAFVGCFAAAM-LARREYLYLGLLSSGVSL 159
DB 161 GEVKGFRANWTVYVSAIFFISLIVLSCGDF-----RKHPNWLVALSILT- 209
QY 160 LFWLHFASSIFGSGMAVF---KFELYF---GLLVFVGYIVFDTEII--EKALHGMNDY 210
DB 267 LF-----IF-AILCIFIRNRILEIVVASLGALLFTCFLAVDTQLLGNKQLSLSPEEY 318
QY 211 VKHALTLFTDFGAVFVRILIM 232
DB 319 VFAALNLYTDIINIFLYLTII 340

RESULT 13
US-08-749-289-3
; Sequence 3, Application US/08749289
; Patent No. 595301
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Coleman, Roger
; TITLE OF INVENTION: NOVEL HUMAN GLUTAMATE-BINDING
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,289
; FILING DATE: Filed Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0160 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 855-0555
; TELEFAX: (415) 845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 516 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-749-289-3

Query Match 7.4%; Score 94.5; DB 2; Length 516;

Best Local Similarity 21.4%; Pred. No. 0.014;
Matches 56; Conservative 48; Mismatches 95; Indels 63; Gaps 14;
QY 2 EGFSPFDSQASRNRWSYSLKXFRQISPLVQTHLKQVYLTLCAL-VASAAGAYLHL 60
DB 111 EGPSPYDNDQFPNVND-----KSIR-----QAFIRKVFVLTLQSLVTSTVAITFFV 160
QY 61 WNIGGL-----LTTMACGSMWMLLSAPPYQEQKRVALLMAALFEG 102
DB 161 GEVKGFRANWTVYVSAIFFISLIVLSCGDF-----RKHPNWLVALSILT- 209
QY 103 ASIGPLIELGINF--DPSIVFGAFVGCFAAAM-LARREYLYLGLLSSGVSL 159
DB 210 ISLSYMGMIASFYNTAEVIMAVGITTA---CFTVVFISMOTRYDFTSCMGVLLSVVV 266
QY 160 LFWLHFASSIFGSGMAVF---KFELYF---GLLVFVGYIVFDTEII--EKALHGMNDY 210
DB 267 LF-----IF-AILCIFIRNRILEIVVASLGALLFTCFLAVDTQLLGNKQLSLSPEEY 318
QY 211 VKHALTLFTDFGAVFVRILIM 232
DB 319 VFAALNLYTDIINIFLYLTII 340

RESULT 14
US-09-372-422A-26
; Sequence 26, Application US/09372422A
; Patent No. 6313375
; GENERAL INFORMATION:
; APPLICANT: Rudolf Jung
; APPLICANT: Francois Barrieu
; TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
; FILE REFERENCE: 0919
; CURRENT APPLICATION NUMBER: US/09/372,422A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: US 60/098,692
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Zea mays
US-09-372-422A-26

Query Match 7.4%; Score 94; DB 4; Length 272;
Best Local Similarity 22.6%; Pred. No. 0.0067;
Matches 48; Conservative 32; Mismatches 70; Indels 62; Gaps 9;
QY 32 LVQTHLKQVYLTLCOA---LVASAAGAYLHLNIGLLTTMACGSMWMLLSAPPYQEQ 88
DB 97 MYRGHITKLRVLYVAAQLASSAACVLLRFL--SGMVTFVHALGRGI-----SPMOGL 149
QY 89 KEVALLMAALF-----EGASIGPLIELGINFDPISIVFGAFVGC-AVVFQCFSA 136
DB 150 VNEVILTFSLFVYVAMLDPRSQVRAIGPLLT-----GLIVGANSIAGNFTG 198
QY 137 AAMLARREYLYLGLLSSGVSLFLWLHFASSIFGSGMAVKFELYFGLLVFVGYIVFD 196
DB 199 ASMPNARS---FGPALATGDWNTNHWVYVWIGPLLGGLAGFVYESLF-----241
QY 197 QELIEKAHLGDMY-----VKEALTLF 218
DB 242 ---LVOKMHEAAQMGSLTTSIPCVVAHASCILF 271

RESULT 15
US-07-879-617A-12
; Sequence 12, Application US/07879617A
; Patent No. 5580775
; GENERAL INFORMATION:
; APPLICANT: Fremieu Jr., Robert T.
; APPLICANT: Caron, Marc G.

APPLICANT: Blakely, Randy D.
TITLE OF INVENTION: A High Affinity L-Proline Transporter
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
ZIP: 30309
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/879,617A
FILING DATE: 19920501
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patricia L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: EMU109
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-815-6508
TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 607 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Rattus
TISSUE TYPE: Brain - serotonin transporter
FEATURE:
NAME/KEY: Active-site
LOCATION: 95..96
OTHER INFORMATION: /note= "Leucine zipper motif"
FEATURE:
NAME/KEY: Active-site
LOCATION: 102..103
OTHER INFORMATION: /note= "Leucine zipper motif"
FEATURE:
NAME/KEY: Active-site
LOCATION: 109..110
OTHER INFORMATION: /note= "Leucine zipper motif"
FEATURE:
NAME/KEY: Active-site
LOCATION: 116..117
OTHER INFORMATION: /note= "Leucine zipper motif"

US-07-879-617A-12
Query Match 6.8%; Score 87; DB 1; Length 607;
Best Local Similarity 22.7%; Pred. No. 0.14; Mismatches 64; Indels 94; Gaps 15;
Matches 55; Conservative 29;
QY 16 NRWSYDSLKNF-----RQISPLVQTHLKQV-----YLTICCAL 48
DB 179 NSWNTGNTNYAQDNITWTLHSTSPAEFYLRHVLIHQSKGLQDLGTTISWQLTLCIVL 238
QY 49 VASAAGAYLHILNIGGLTTMACGSMVLLSAPPYQEQKRVALLMAALFEGASIGPL 108
DB 239 IFTV--IYPSI-WK--GVATIS---GKVWWTATFPY-----IVLSVLLVRGATL--- 279
QY 109 IELGINFDPISIVFGAFVGCVAVFGFSAAMLARRELYYL-----GGLSSGVSLLEWHL 164
DB 280 -----FGAWRG--VVF-----YLPKNWQKLLETGV-----WVD 305

QY 165 PASSIFGSGMAVFKPELYFG-LLNVFVGIVYEDT---QELIEKAHLGDMDVVKHALTILFTD 220
DB 306 AAAQIF-----FSLGPGFGVLLAPASINKFNNNCYQDALVTSVNNCNTSFVSGFVIFTV 359
QY 221 FG 222
DB 360 LG 361
Search completed: May 25, 2003, 12:24:35
Job time : 37 secs

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OM protein - protein research, using sw model

Run on: May 25, 2003, 12:22:59 ; Search time 54 Seconds
(without alignments)
455.460 Million cell updates/sec

Title: US-09-955-526-4
Perfect score: 1272
Sequence: 1 MEGTSPFDQSASRNWSY.....LIIMLNKXSEKKEKKRN 248

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 375593 seqs, 99172665 residues

Total number of hits satisfying chosen parameters: 375593

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pap.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pap.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pap.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pap.*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pap.*
 - 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pap.*
 - 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pap.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pap.*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pap.*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pap.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pap.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pap.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pap.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1272	100.0	248	9	US-09-955-526-4
2	988	77.7	244	9	US-10-167-015-16
3	963.5	75.7	247	9	US-10-219-220-274
4	955	75.1	261	9	US-10-167-015-18
5	884.5	69.5	252	9	US-10-167-015-32
6	878.5	69.1	258	9	US-10-167-015-34
7	878.5	69.1	285	9	US-10-167-015-6
8	853	67.1	252	9	US-10-167-015-4
9	786.5	61.8	250	9	US-10-167-015-2
10	772.5	60.7	255	9	US-10-219-220-273
11	688.5	54.1	213	9	US-10-219-220-87
12	499.5	39.3	140	9	US-10-167-015-8
13	484.5	38.0	141	9	US-10-219-220-88
14	483.5	38.1	255	10	US-09-925-302-516
15	339	26.7	78	9	US-10-167-015-20
16	165	13.0	345	9	US-09-992-598-2
17	165	13.0	345	9	US-09-989-293A-2
18	165	13.0	345	9	US-09-989-735-2
19	165	13.0	345	9	US-09-990-444-2

ALIGNMENTS

RESULT 1

US-09-955-526-4

; Sequence 4, Application US/09955526

; Publication No. US20030009785A1

; GENERAL INFORMATION:

; APPLICANT: Reed, John C.

; TITLE OF INVENTION: Plant Cytoprotective Genes and Methods

; FILE OF INVENTION: of Using Same

; FILE REFERENCE: P-LJ 4868

; CURRENT APPLICATION NUMBER: US/09/955,526

; CURRENT FILING DATE: 2001-09-12

; PRIOR APPLICATION NUMBER: US 09/661,014

; PRIOR FILING DATE: 2000-09-13

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 248

; TYPE: PRT

; ORGANISM: Lycopersicon esculentum

US-09-955-526-4

Query Match 100.0%; Score 1272; DB 9; Length 248;

Best Local Similarity 100.0%; Pred. No. 5.4e-115;

Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEGFTSPFDQSASRNWSYDSLKNFRQISPLVQTHLKQVYTLCCALVASAAGAYLHIL	60
DB	1	MEGFTSPFDQSASRNWSYDSLKNFRQISPLVQTHLKQVYTLCCALVASAAGAYLHIL	60
QY	61	WNIGLLTTMACSGSMVWLLSAPPYQCKRVALLMAALFEGASIGPLIELGINFDPISIV	120
DB	61	WNIGLLTTMACSGSMVWLLSAPPYQCKRVALLMAALFEGASIGPLIELGINFDPISIV	120
QY	121	FCAGVGCNAVFGCFSAAAMLARREYLYLGLSSGVSLLFWLHFASSIFGGSMVAFKPE	180
DB	121	FCAGVGCNAVFGCFSAAAMLARREYLYLGLSSGVSLLFWLHFASSIFGGSMVAFKPE	180
QY	181	LYFGLLVFGVIVFTQBIIEKAHLGMDYVVKHALTFTDFGAVFVRILLIMLNKASEKE	240
DB	181	LYFGLLVFGVIVFTQBIIEKAHLGMDYVVKHALTFTDFGAVFVRILLIMLNKASEKE	240
QY	241	EKKXERN	248

Db 241 EKKKKRN 248
|||||

RESULT 2

US-10-167-015-16
; Sequence 16, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Jchal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Glycine max
US-10-167-015-16

Query Match 77.7%; Score 988; DB 9; Length 244;
Best Local Similarity 75.5%; Pred. No. 1.3e-87;
Matches 185; Conservative 32; Mismatches 24; Indels 4; Gaps 1;

QY 4 FTSPFDSQSRNWSYDLSKNFRQISPLVQTHLKOVYTLCCALVASAAGAYLHLWNI 63
Db 4 FNSFFD-----SRNRWYDTLKNFRQISPVVQNHKLKOVYTLCCALVASAAGAYLHLWNI 59
QY 64 GGLTTMACGSMVWLLSAPPYQEQKRVALLMAALFEGASIGPLIELGINFDPDSIVFGA 123
Db 60 GGLTTVACMGSSFWLLSTPPEERKRVLLMAALFQGSIGPLIELGINFDPDSIVFGA 119
QY 124 FVGCNAVFCFSAAMARREYLYLGGSSVSLFLFHLFASIFGGSMAVFKFELYF 183
Db 120 FVGCNAVFCFSAAMARREYLYLGGSSVSLFLFHLFASIFGGSMAVFKFELYF 179
QY 184 GLLVFGYIVFTQEIIEKAHLGDMYVVKHALTFTDFGAVFVRILIMLKNASEKKEK 243
Db 180 GLLVFGYIVFTQEIIEKAHLGDMYVVKHALTFTDFGAVFVRILIMLKNASEKKEK 239
QY 244 KRRN 248
Db 240 KRRD 244
|||||

RESULT 3

US-10-219-220-274
; Sequence 274, Application US/10219220
; Publication No. US20030082724A1
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of plant development
; FILE REFERENCE: 11600.1022c1
; CURRENT APPLICATION NUMBER: US/10/219,220
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 274
; LENGTH: 247
; TYPE: PRT

; ORGANISM: Eucalyptus grandis
US-10-219-220-274

Query Match 75.7%; Score 963.5; DB 9; Length 247;
Best Local Similarity 74.4%; Pred. No. 3.1e-85;
Matches 186; Conservative 27; Mismatches 32; Indels 5; Gaps 2;
QY 1 MEGTFTFFDSQSRNWSYDLSKNFRQISPLVQTHLKOVYTLCCALVASAAGAYLHLWNI 60
Db 1 MDAFASLFQS---SGKWSHDSLNFRQISPAVQSHLKNVYLSLCCALMASAGAYLHLWNI 57
QY 61 WNIIGLLTTMACGSMVWLLSAPPYQEQKRVALLMAALFEGASIGPLIELGINFDPDSIV 120
Db 58 WNIIGLLTTMACGSMVWLLSAPPYQEQKRVALLMAALFEGASIGPLIELGINFDPDSIV 117
QY 121 FVGCNAVFCFSAAMARREYLYLGGSSVSLFLFHLFASIFGGSMAVFKFELYF 180
Db 118 ISAFVGSALAFACFSAAMARREYLYLGGSSVSLFLFHLFASIFGGSMAVFKFELYF 177
QY 181 LYFGLLVFGYIVFTQEIIEKAHLGDMYVVKHALTFTDFGAVFVRILIMLKNASEKE 240
Db 178 LYFGLLVFGYIVFTQEIIEKAHLGDMYVVKHALTFTDFGAVFVRILIMLKNASEKE 237
QY 241 --EKKKKRN 248
Db 238 KNEKKKKRRD 247
|||||

RESULT 4

US-10-167-015-18
; Sequence 18, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Jchal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Glycine max
US-10-167-015-18

Query Match 75.1%; Score 955; DB 9; Length 261;
Best Local Similarity 73.3%; Pred. No. 2.2e-84;
Matches 178; Conservative 36; Mismatches 27; Indels 2; Gaps 1;

QY 6 SPEDSQ--SASRNWSYDLSKNFRQISPLVQTHLKOVYTLCCALVASAAGAYLHLWNI 63
Db 3 TPNSSOSSSSRSRWSYDLSKNFRQISPLVQTHLKOVYTLCCALVASAAGAYLHLWNI 62
QY 64 GGLTTMACGSMVWLLSAPPYQEQKRVALLMAALFEGASIGPLIELGINFDPDSIVFGA 123
Db 63 GGLTTTLAGISGSMVWLLSTPPEERKRVLLMAALFQGSIGPLIELGINFDPDSIVFGA 122
QY 124 FVGCNAVFCFSAAMARREYLYLGGSSVSLFLFHLFASIFGGSMAVFKFELYF 183
Db 123 FVATSLAFACFSAAMARREYLYLGGSSVSLFLFHLFASIFGGSMAVFKFELYF 182
QY 184 GLLVFGYIVFTQEIIEKAHLGDMYVVKHALTFTDFGAVFVRILIMLKNASEKKEK 243
Db 183 GLLVFGYIVFTQEIIEKAHLGDMYVVKHALTFTDFGAVFVRILIMLKNASEKKEK 242
|||||

QY 244 KKR 246
Db 243 KKR 245

RESULT 5

US-10-167-015-32
; Sequence 32, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Zea mays
US-10-167-015-32

Query Match 69.5%; Score 884.5; DB 9; Length 252;

Best Local Similarity 66.4%; Pred. No. 1.3e-77;
Matches 166; Conservative 36; Mismatches 41; Indels 7; Gaps 2;

QY 6 SFDDQSAS-----NRWSYSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHI 59
Db 3 AFPSASAPYCGAGWSYSLKNFRQITAVQTHLKVYLTLCCALVASAVGAYLHV 62
QY 60 LWNIGLLTMACGSMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIELGI 119
Db 63 VMNIGTLMGCVGSIWLFSPVYERKRYLLMAAALLEGASVGLVLAFFDPSI 122
QY 120 VFCAFVGCVAFFCFSAAMARREYLYLGLSSGVSLFLFWLHFASISFGGSMVAFKF 179
Db 123 LVTFVGTATACFTCAAWARREYLYLGLSSGVSLILMLQAGSIFGHSATSPMF 182
QY 180 ELYFGLLVFGYIVFTDQBIIEKAHLGDMYVVKHALTLFTDFGAVFVRILIMLNASEK 239
Db 183 EVYFGLLVFGYIVFTDQBIIEKAHLGDMYVVKHALTLFTDFGAVFVRILIMLNASEK 242

QY 240 -BEKKKKRN 248
Db 243 SEDKKKKRS 252

RESULT 6

US-10-167-015-34
; Sequence 34, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Zea mays
US-10-167-015-34

Query Match 69.1%; Score 878.5; DB 9; Length 258;

Best Local Similarity 65.8%; Pred. No. 5.2e-77;
Matches 169; Conservative 37; Mismatches 42; Indels 9; Gaps 3;

QY 1 MEGFTSFDDQSASR-----NRWSYSLKNFRQISPLVQTHLKQVYLTLCCALVASAA 53
Db 1 MDAFYSTTASSSTSSAPYGGGEGWYDSMKNFQISPAVQTHLKVYLTLCCALVASAV 60
QY 54 GAYLHILWNIGLLTMACGSMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIELGI 113
Db 61 GAYLHVWNIGLLTMACGSMVWLLSAPPYQEQKRVALLMAAALLEGASVGLIKLAV 120
QY 114 NPDPISIVFGAVGCVAFVGCPSAAAMARREYLYLGLSSGVSLFLFWLHFASISFG-G 172
Db 121 EFDPSILVTFVGTATACFTCAAWARREYLYLGLSSGVSLILMLQAGSIFGHSATSPMF 180
QY 173 SMAYEKEELYFGLLVFGYIVFTDQBIIEKAHLGDMYVVKHALTLFTDFGAVFVRILIM 232
Db 181 STSSFMFEVIFGLLVFGYIVFTDQBIIEKAHLGDMYVVKHALTLFTDFGAVFVRILIM 240
QY 233 LKNASEK-BEKKKKRN 248
Db 241 LKNAADKSEDKKKRS 257

RESULT 7

US-10-167-015-6
; Sequence 6, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Zea mays
US-10-167-015-6

Query Match 69.1%; Score 878.5; DB 9; Length 285;

Best Local Similarity 65.8%; Pred. No. 5.8e-77;
Matches 169; Conservative 37; Mismatches 42; Indels 9; Gaps 3;

QY 1 MEGFTSFDDQSASR-----NRWSYSLKNFRQISPLVQTHLKQVYLTLCCALVASAA 53
Db 1 MDAFYSTTASSSTSSAPYGGGEGWYDSMKNFQISPAVQTHLKVYLTLCCALVASAV 60
QY 54 GAYLHILWNIGLLTMACGSMVWLLSAPPYQEQKRVALLMAAALFEGASIGPLIELGI 113
Db 61 GAYLHVWNIGLLTMACGSMVWLLSAPPYQEQKRVALLMAAALLEGASVGLIKLAV 120
QY 114 NPDPISIVFGAVGCVAFVGCPSAAAMARREYLYLGLSSGVSLFLFWLHFASISFG-G 172
Db 121 EFDPSILVTFVGTATACFTCAAWARREYLYLGLSSGVSLILMLQAGSIFGHSATSPMF 180

QY 175 AVFKEFLVGLVFGYIVFDTOETIEKAHLGDMYVVKHALTLFTDFGAVFVRILIMLK 234
DB 181 AYTETVFGLLVFGYIVFDTOETIEKAHLGDMYVVKHALTLFTDFGAVFVRILIMLK 240
QY 235 NA-SEKEKKKKRR 247
DB 241 NADSKSREGKKRR 254

RESULT 11
US-10-219-220-87
; Sequence 87, Application US/10219220
; Publication No. US20030082724A1
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: Death and their use in the modification of plant development
; FILE REFERENCE: 11000.1022c1
; CURRENT APPLICATION NUMBER: US/10/219,220
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 87
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Pinus radiata
US-10-219-220-87

Query Match 54.1%; Score 688.5; DB 9; Length 213;
Best Local Similarity 64.6%; Pred. No. 8.8e-59;
Matches 137; Conservative 31; Mismatches 41; Indels 3; Gaps 2;

QY 39 QVYLTCCALVASAGAYLHILNIGGLTTMACGSMVLLSAP--PYOEQKREKALLMA 96
DB 1 RYLSLSALVTAALGVYHLLNIGGLTGLACIGSVIGLLSVPTSSNNEKGAALLA 60

QY 97 AALFEGASIGPIELGIFNPDPSVFGAVGCVFVGCPSAAAMLARRREYLYIGLLSSG 156
DB 61 AAFAFGATGLPLIDAVINIDSSILVSFAVGTSLAFACPSAAAITARRREYLYIGLLSSG 120

QY 157 VSLFWLHFASSIFGSMVAVKPELYFGLLVFGYIVFDTOETIEKAHLGDMYVVKHALT 216
DB 121 ISILMWQLASSIFGSSAIYTFEYFGLLVFGYIVFDTOETIEKAHLGDMYVVKHALT 180

QY 217 LFTDFGAVFVRILIMLNA-SEKEKKKKRR 247
DB 181 LFTDFGAVFVRILIMLNA-SEKEKKKKRR 212

RESULT 12
US-10-219-220-88
; Sequence 88, Application US/10219220
; Publication No. US20030082724A1
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: Death and their use in the modification of plant development
; FILE REFERENCE: 11000.1022c1
; CURRENT APPLICATION NUMBER: US/10/219,220
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 88
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Pinus radiata

US-10-219-220-88

Query Match 39.3%; Score 499.5; DB 9; Length 140;
Best Local Similarity 56.2%; Pred. No. 9.1e-41;
Matches 100; Conservative 14; Mismatches 26; Indels 11; Gaps 2;

QY 1 MEGFTSPFDSQASRNWSYDSLKNFRQISPLVOTHLKQVYLTCCALVASAGAYLHIL 60
DB 1 MDAFASLFSQ---SGKGWSDSLKNFRQISPAVQSHLKNVYLSLCCALMASAGAYLHIL 57

QY 61 WNIGGLTTMACGSMVLLSAPPYQOEKREKALLMAALFEGASIGPIELGIFNPDPSIV 120
DB 58 LNIGGLTTIACIGSVLLLSIPHEEQKREKALLMAALFEGASIGPIELGIFNPDPSIV 117

QY 121 FGAIVGCAVVGCFSAAMLARRREYLYLGG 151
DB 118 ISAFVGSALAFACFSGAA-----CWLOGG 140

RESULT 13

US-10-167-015-8
; Sequence 8, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 141
; TYPE: PRT
; ORGANISM: zea mays
US-10-167-015-8

Query Match 38.1%; Score 484.5; DB 9; Length 141;
Best Local Similarity 57.4%; Pred. No. 2.6e-39;
Matches 93; Conservative 21; Mismatches 23; Indels 1; Gaps 1;

QY 112 GINFDPSIVFGAVGCAVVGCFSAAMLARRREYLYLGGLLSSGVLFWLHFASSIFG 171
DB 4 GCFSSLSILVTAFAVGTAFACFTGAAMVARREYLYLGGLLSSGVLFWLHFASSIFG 63

QY 172 GSMVAVKPELYFGLLVFGYIVFDTOETIEKAHLGDMYVVKHALTLFTDFGAVFVRILII 231
DB 64 HSATSFMEVYFGLLIFGVYVYDTQETIIEAHRGDMYVVKHALTLFTDFGAVFVRILII 123

QY 232 MLKNASEK-EKCKKKRR 248
DB 124 MLKNGADKSEKCKKKRS 141

RESULT 14

US-09-925-302-516
; Sequence 516, Application US/09925302
; Patent No. US2002004941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08

Search completed: May 25, 2003, 12:31:16
Job time : 55 secs

```
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 516
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-516

Query Match      38.0%; Score 483.5; DB 10; Length 255;
Best Local Similarity 41.1%; Pred.No. 6.5e-39;
Matches 102; Conservative 54; Mismatches 79; Indels 13; Gaps 5;

QY 3 GFTSFFDSQASNRNWSYSLKQNPQISPLVQTHLKQVYLTCCALVASAGAYLHILWN 62
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 17 GTWNIFD-----RKINFDAALXFSHTPTQOHLKKVYASFALCMFVAAGAYVHMVTH 70
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 63 I--GGLLTTWACGSMYWLISAPPYQ--EOKRVALLMAAALFEGASIGPLIELGINFOPS 118
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 71 FIQAGLLSALGSLILMLWATPHSHETEQKRLGGLAGFAFLTGVLGPALEFCIAVNP 130
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 119 IVFGAFVGCVAVFCFSAAMLAARRBYLYLGGLLSGVSLFLFWLHFASIFGGSMAVFK 178
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 131 ILPTAFMGTAIFTCFTLSALYARRSYLFLGGLMSALL--LSSLGNVFFGSIWLFQ 189
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 179 FELYGLLVFGYIVFDTQELIEKAHLGDMDYVKHALTLFTDFGAVFVRILIMLNASE 238
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 190 ANLYVGLVVMCGFVFDITQILIEKAHGDQDIYWHCIDLFLDEITVFRKMLMLAN--E 247
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 239 KEEKKKR 246
   | : | : | :
Db 248 KDKKKKK 255
   | : | : | :

RESULT 15
US-10-167-015-20
; Sequence 20, Application US/10167015
; Publication No. US20030056249A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Johal, Gurmukh
; APPLICANT: Acevedo, Pedro A. Navarro
; APPLICANT: Tao, Yumin
; TITLE OF INVENTION: Anti-Apoptosis Genes and Methods of Use
; FILE REFERENCE: 1388
; CURRENT APPLICATION NUMBER: US/10/167,015
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/297,478
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 78
; TYPE: PRT
; ORGANISM: glycine max
US-10-167-015-20

Query Match      26.7%; Score 339; DB 9; Length 78;
Best Local Similarity 80.8%; Pred.No. 1.4e-25;
Matches 63; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 171 GGSMAVEKFEYFGLLVFGYIVFDTQELIEKAHLGDMDYVKHALTLFTDFGAVFVRILI 230
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1 GGSIALFRFELYFGLLVFGYIVFDTQELIERAFGLDLYVKHALTLFTDLAIFVRILI 60
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 231 IMLKNASEKEKKKKRN 248
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 61 IMLKNSERNKKKKRD 78
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
```

GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2003, 12:16:44 ; Search time 43 Seconds
(without alignments)
554.450 Million cell updates/sec

Title: US-09-955-526-4

Perfect score: 1272

Sequence: 1 MEGTSPFDSQSASRNWSY.....LIIMKNASEKEKKKKRN 248

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 73:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1023.5	80.5	247	T52449	Bax inhibitor-1 (i
2	479	37.7	236	S42069	TEGT protein - rat
3	472	37.1	261	E71445	hypothetical prote
4	472	37.1	262	A85197	TEGT protein homol
5	471.5	37.1	237	I38334	TEGT (testis enhan
6	170.5	13.4	219	A10628	probable membrane
7	157.5	12.4	219	D85624	probable carrier/t
8	157.5	12.4	219	F90760	probable glutamate
9	157.5	12.4	219	S07180	probable receptor-
10	144	11.3	266	T41414	hypothetical prote
11	143.5	11.3	342	T34438	probable membrane
12	143	11.2	297	S33281	integral membrane
13	136.5	10.7	245	S3484	conserved hypothet
14	130.5	10.3	238	E81729	probable transpor
15	128.5	10.1	238	E71457	probable membrane
16	128	10.1	236	A10142	hypothetical prote
17	124.5	9.8	239	T48120	conserved hypothet
18	124	9.7	231	A75422	probable integral
19	123.5	9.7	231	D81441	ybHL protein - Esc
20	122	9.6	234	B48415	hypothetical prote
21	122	9.6	234	H90736	hypothetical prote
22	122	9.6	234	A85587	hypothetical prote
23	121.5	9.6	239	Q08EGS	HWLF2 protein - hu
24	120	9.4	222	S38835	probable glutamate
25	120	9.4	222	H24489	hypothetical prote
26	114.5	9.0	220	A44141	probable glutamate
27	114	9.0	227	G81014	conserved hypothet
28	113	8.9	223	D82210	conserved hypothet
29	112.5	8.8	230	H54634	conserved hypothet

30	112	8.8	232	2	AH0954	probable membrane
31	109.5	8.6	230	2	F71879	hypothetical prote
32	109	8.6	260	2	B97681	hypothetical prote
33	109	8.6	260	2	A12905	conserved hypothet
34	108.5	8.5	236	2	H71724	hypothetical prote
35	106	8.3	659	2	AB1293	ABC transporter (p
36	104	8.2	203	2	S53708	N-methyl-D-aspart
37	103.5	8.1	670	2	AH1664	ABC transporter (p
38	101.5	8.0	225	2	AG1350	hypothetical prote
39	101.5	8.0	236	2	E97723	hypothetical prote
40	101.5	8.0	238	2	H86611	transport permease
41	101.5	8.0	238	2	A72013	transport permease
42	99.5	7.8	225	2	AB1721	hypothetical prote
43	99.5	7.8	248	2	T01080	hypothetical prote
44	99	7.8	231	2	D97248	conserved membrane
45	98.5	7.7	511	2	JC7692	oligodendrocyte tr

ALIGNMENTS

RESULT 1

T52449

Bax inhibitor-1 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 03-Nov-2000

C:Accession: T52449

R:Kawai, M.; Pan, L.; Reed, J.C.; Uchimiya, H.

FEBS Lett. 464, 143-147, 1999

A:Title: Evolutionally conserved plant homologue of the Bax Inhibitor-1 (BI-1) gene car

A:Reference number: Z26078

A:Accession: T52449

A:Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-247 <RAW>

A:Cross-references: EMBL:AB025927; PIDN:BA089541.2

A:Experimental source: cultivar Columbia

C:Genetics:

A:Gene: AtBI-1

C:Function:

A:Description: suppresses cell death induced by Bax

C:Superfamily: human testicular protein TEGT

Query Match 80.5%; Score 1023.5; DB 2; Length 247;

Best Local Similarity 77.4%; Pred. No. 1.4e-85;

Matches 192; Conservative 31; Mismatches 24; Indels 1; Gaps 1;

Qy 1 MEGTSPFDSQSASRNWSYDSLKNFQISPLVQTHLKQVYLTLCALVASAGAYLHL 60

Db 1 MDAFSSPFDSQFSGRS-WSYDSLKNFQISPAVQNLKRVYLTLCALVASAGAYLHL 59

Qy 61 WNIGGLTITMACMGSVMYLLSAPPYQKQKVALMAALFEGASIGLIELGINFDPSTV 120

Db 60 WNIGGLTITGICGTMIWLLSCPPYEHQKLSLLFVSAVLEGASVGLIKVAIDVDPSIL 119

Qy 121 FGAFGCCAVFGCCSAAMLARREYLYLGLSSGVSLFLFWLHPASSIFGGSMVFKKE 180

Db 120 ITAFVGTATAPVCSAAMLARREYLYLGLSSGVSLMLMQLQFASSIFGGSSAFKKE 179

Qy 181 LYFGLLVFGYIVDFDTQEIIEKAHLGDMYVVKHALTFDFGAVFVRIRIILIMKNASEKE 240

Db 180 LYFGLLVFGYVVDVDTQEIIEKAHLGDMYVVKHSLTFDFVAVFVRIRIILIMKNASADKE 239

Qy 241 EKKKKRN 248

Db 240 EKKKKRN 247

RESULT 2

S42069

TEGT protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

Query Match 37.1%; Score 472; DB 2; Length 261;

```
Query Match 37.1%; Score 471.5; DB 2; Length 237;
Best Local Similarity 42.2%; Pred. No. 1.9e-35;
Matches 98; Conservative 51; Mismatches 76; Indels 7; Gaps 4;

QY 19 SYDSLKFRQISPLVQTHLKQVYLTLCALVASAGAYLHILWNI--GGLTTWACGSM 76
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 9 NFDALLKFSHTPTQQHLKKVYAFALCMFAAGAYVMVTHFIQAGLLSALGSLIM 68
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 77 VMLLSAPPYQ--EQRVALLMAALFEGASIGPLIELGINFDPISVFGAFVGCVF 134
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 69 INLMATPSHETEQRKGLLAGFAFLTGVGIGPALEFCIAVNPISILPTAWGTAMITCF 128
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 135 SAAMALARREYLYLGGILSSGVSLFLWHPASSIFGSGMAVFKFELYGLLVFGVYVIF 194
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 129 TLSALYARRSYFLFGILMSALSLL--LSSLGNVFFGSIPFQANLYNGLVVMCGFVLV 187
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 195 DTQEIIEKAHLGDMYVVKHALTFTDFGAVFVRIILIIMLKVASKEKKKKR 246
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 188 DTQLIIEKAHGDQYIWHCIDLDFLDFITVRKLMMLAMN--EKDKKKKK 237
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 6
A:Title: Membrane protein STY112 [imported] - Salmonella enterica serov
A:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: This species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 02-Aug-2002
C:Accession: A10628
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Garra, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; PMID:11677608
A:Accession: A10628
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-219 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD08212.1; PID:G16502260; GSPDB:GN00176
C:Genetics:
A:Gene: STY112
C:Superfamily: Escherichia coli ybhL protein

Query Match 13.4%; Score 170.5; DB 2; Length 219;
Best Local Similarity 29.2%; Pred. No. 3.9e-08;
Matches 66; Conservative 42; Mismatches 77; Indels 41; Gaps 11;

QY 27 ROISPLVQTH--LKQVY--LTLCCALVASAGAYLHILWNI--GGLTTWACGSMVLLSA 82
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 9 RDRSLLSTHKVLRNTYFLLSLTAFSAITATASTVLMPLSPGILTLVGMVGLMFL-- 65
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 83 PPYQ--EQRVALLMAAL--FEGASIGPLIELGINFDPISVFG--AFVGCVAVFGCFSA 138
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 66 --TYKTANKPVGILSAFAFTGFGYILGILNAYLSAGMDVIGALGGLTALVFCCS--AY 123
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 139 MLARREYLYLGGILSSGVSLFL--FEGASIGPLIELGINFDPISVFG--AFVGCVAVFG 186
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 124 VLTTRKDSFLGGLMAGIVVYLVIGWVNIQLPALHLAIS-----AVF-----IL 170
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 187 VFVGYIVFTQRIIEKAHLGDMYVVKHALTFTDFGAVFVRIILIIM 232
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 171 ISSGALLYFETSNII--HGGEINIRATVSVLYSVLYNIFVSLLSIL 213
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 7
A:Title: Membrane protein ybhL protein yccA [imported] - Escherichia coli (strain O157:H7, s
A:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Aug-2002
C:Accession: D85624
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: AB5480; MUID:21074935; PMID:11206551
A:Accession: D85624
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-219 <STO>
A:Cross-references: GB:AE005174; NID:G12514158; PIDN:AAG55456.1; GSPDB:GN00145; UWGP:Z1
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: yccA
C:Superfamily: Escherichia coli ybhL protein

Query Match 12.4%; Score 157.5; DB 2; Length 219;
Best Local Similarity 26.7%; Pred. No. 5.9e-07;
Matches 64; Conservative 45; Mismatches 80; Indels 51; Gaps 11;

QY 12 SASNRWSYDLSKNFRQISPLVQTH--LKQVY--LTLCCALVASAGAYLHILWNI--GGLL 67
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 6 SSSHDRTS-----LLSTHKVLRNTYFLLSLTAFSAITATASTVLMPLSPGLI 53
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 68 TTMACGSMVWLLSAPPYQOKRVALLMAAL--FEGASIGPLIELGINFDPISVFGAF 124
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 54 LTLVGMVGLMFLTYK--MANKPTGIISAFATGFLGYILGILPILTYLSAGMGDVIALM 110
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 125 VGCVAVFGCFSAAMALARREYLYLGGILSSGVSLFL--FEGASIGPLIELGINFDPISVFG 172
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 111 GGTALVFFCCS--AVLTTRKDSFLGGLMAGIVVYLVIGWVNIQLPALHLAIS----- 165
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 173 SMVAFKELYLGLLVFGVYIVFTQRIIEKAHLGDMYVVKHALTFTDFGAVFVRIILIIM 232
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 166 --AVF-----ILISSGAILFETSNII--HGGEINIRATVSVLYSVLYNIFVSLLSIL 213
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 8
F90760
A:Title: probable carrier/transport protein ECs1054 [imported] - Escherichia coli (strain O157:H7,
A:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Aug-2002
C:Accession: F90760
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.C
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and ger
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F90760
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-219 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA034477.1; PID:G13360514; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECs1054
C:Superfamily: Escherichia coli ybhL protein

Query Match 12.4%; Score 157.5; DB 2; Length 219;
Best Local Similarity 26.7%; Pred. No. 5.9e-07;
Matches 64; Conservative 45; Mismatches 80; Indels 51; Gaps 11;

QY 12 SASNRWSYDLSKNFRQISPLVQTH--LKQVY--LTLCCALVASAGAYLHILWNI--GGLL 67
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 6 SSSHDRTS-----LLSTHKVLRNTYFLLSLTAFSAITATASTVLMPLSPGLI 53
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 68 TTMACGSMVWLLSAPPYQOKRVALLMAAL--FEGASIGPLIELGINFDPISVFGAF 124
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 54 LTLVGMVGLMFLTYK--MANKPTGIISAFATGFLGYILGILPILTYLSAGMGDVIALM 110
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 125 VGCVAVFGCFSAAMALARREYLYLGGILSSGVSLFL--FEGASIGPLIELGINFDPISVFGAF 172
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 111 GGTALVFFCCS--AVLTTRKDSFLGGLMAGIVVYLVIGWVNIQLPALHLAIS----- 165
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 173 SMVAFKELYLGLLVFGVYIVFTQRIIEKAHLGDMYVVKHALTFTDFGAVFVRIILIIM 232
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
```


Db 166 --AVF-----ILISSGALLPETSNI---HGGETNYIRATVSLVSLYNIFVSLLSIL 213

RESULT 9
S07180
Probable glutamate receptor ycca - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 01-Mar-2002
C:Accession: S07180; A64838
R:Ramura, F.; Nishimura, S.; Ohki, M.
EMBO J. 3, 1103-1107, 1984
A:Title: The E. coli divE mutation, which differentially inhibits synthesis of certain P
A:Reference number: S07180; PMID:84236106; PMID:6376117
A:Accession: S07180
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-219 <TAM>
A:Cross-references: EMBL:X00547; NID:g41283; PIDN:CAA25218.1; PID:g41284
A:Experimental source: strain W3110
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; PMID:97426617; PMID:9278503
A:Accession: A64838
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-219 <BLAT>
A:Cross-references: GB:AE000199; GB:U00096; NID:g1787202; PIDN:AAC74056.1; PID:g1787205;
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: ycca
A:Map position: 22 min
C:Superfamily: Escherichia coli ybhl protein
F:26-42/Domain: transmembrane protein
F:43-59/Domain: transmembrane #status predicted <TM1>
F:75-91/Domain: transmembrane #status predicted <TM2>
F:105-121/Domain: transmembrane #status predicted <TM3>
F:128-154/Domain: transmembrane #status predicted <TM4>
F:162-178/Domain: transmembrane #status predicted <TM5>
F:200-216/Domain: transmembrane #status predicted <TM7>

Query Match 12.4%; Score 157.5; DB 2; Length 219;
Best Local Similarity 27.0%; Pred. No. 5.9e-07;
Matches 65; Conservative 46; Mismatches 77; Indels 53; Gaps 12;

QY 12 SASRNRWSYSLKFRQISPLVQTH--LKQVY--LTLCCALVASAGAYLHLNIGGLL 67
Db 6 SSSHDRTS-----LSTHKLVRNTYFLSLTAFSAITATASTVMLPSPGLI 53

QY 68 TTMACGSMWLLSAPPYQ-EQKRVALLMAAL--FEGASIGFLIELGINFDP-PSIVFGA 123
Db 54 LTLVGMVGLMFL---TYTKANKPTGIIISAFATGFLGVLGPIILNTVLSAGMGDVIA 109

QY 124 FVGCVVFGGCSAAMLARREVLVGLLSSGVSLFP-----WLHPASSIFG 171
Db 110 LGGTALVFFCCS-AYLITTRKMSFLGGLMAGIVVVLGMVANIFLQLPALHLAIS--- 165

QY 172 GSMVAFKFLYFGLVFGVYVFDTCETIEKAHLGDMVDYVKHALFTDFGAVFRIILI 231
Db 166 --AVF-----ILISSGALLPETSNI---HGGETNYIRATVSLVSLYNIFVSLLSI 212

QY 232 M 232
Db 213 L 213

RESULT 10
T41414
Probable receptor-associated protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T41414
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z21954
A:Accession: T41414
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-266 <WOO>
A:Cross-references: EMBL:AL031798; PIDN:CAA21193.1; GSPDB:GN00068; SPDB:SPCC576.04
A:Experimental source: strain 972h-; cosmid C576
C:Genetics:
A:Gene: SPDB:SPCC576.04
A:Map position: 3

Query Match 11.3%; Score 144; DB 2; Length 266;
Best Local Similarity 24.9%; Pred. No. 1.2e-05;
Matches 65; Conservative 39; Mismatches 95; Indels 62; Gaps 14;

QY 10 SOSARNWSYSLKFRQISPLVQ-----THLKQVYLTLCAL-VASAAGA--YLHI 59
Db 29 NESATEN---PAVDQFNKTTTVAECAKSRMAFLRKVYAILTAQLFVTSLFGGIFLHP 84

QY 60 LWN-----IGGLTTMACGSMWLLSAPPYQEKRVALLMAALFEGASIGPL 108
Db 85 AFSFVQVQHPFLLINFFISLVLPF-----LIMKPYSPRYVIFLFLTALEGLTILGTA 139

QY 109 IELGNFDPISIVFGAVGCAVFGCFSA--AAMLARREVLVGLLSSGV-----SLL 160
Db 140 ITF---FSARIILEAVF---ITLGVFVALTAFTQSKWDFSLRGFLYVLSLILTLPLI 193

QY 161 FWL---HFASSIFGSMVAFKFLYFGLVFGVYVFDTCETIEKAHLGDMVDYVKHALT 216
Db 194 FPFVSTPFDMAFAG-----FGTLVFCGIIILFDYINILHR--YSPERFIMSSLM 241

QY 217 LFTDFGAVFRIILI--MLKN 235
Db 242 LYLDINFLFIRILQILGLMLQN 262

RESULT 11
T34438
Hypothetical protein K11H12.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T34438
R:Bradshaw, H.
submitted to the EMBL Data Library, February 1997
A:Description: The sequence of C. elegans cosmid K11H12.
A:Reference number: Z21526
A:Accession: T34438
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-342 <BRA>
A:Cross-references: EMBL:U86168; PIDN:AAC24402.1; GSPDB:GN00022; CESP:K11H12.8
A:Experimental source: strain Bristol N2; clone K11H12
C:Genetics:
A:Gene: CESP:K11H12.8
A:Map position: 4
A:Introns: 45/3; 67/1; 150/3; 186/1; 262/1; 314/2

Query Match 11.3%; Score 143.5; DB 2; Length 342;
Best Local Similarity 23.7%; Pred. No. 1.8e-05;
Matches 51; Conservative 47; Mismatches 86; Indels 31; Gaps 8;

QY 42 LTLCCALVASAGAYLHLNIGGLTTMACGSMWNL-LSAPPYQEKRVALLMAAL- 99
Db 126 LTAVSGVAASRAAIMRLTAG--GGNMSIFGTMAAMIASGMLARSIDYESTVAKELAWALH 184

QY 100 --FEGASIGFLIELGINFDPISIVFGAVGCAVFGCFSAAMLARREVLVGLLSSGV 157
Db 185 CGVLGAVAPLFCFMA---GPVLTAAWYTAGIV--GGSATATAPSEKFLMMSGPLAMGF 240

QY 158 SLLFWLHFAS-----SIFGSMVAFKFLYFGLVFGVYVFDTCETIEKA 203

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Db 241 GVVFVANICAFPLPGSGALGASLA--STVYVGLILFSAFLLYDQRLVKKAENHPHSSQ 298
QY 204 -----HLGDMYVVKHALTFTDFGAVFVRILIM 232
Db 299 LYGSDMQIRSDPINAQMSIYDNLNIPRLVIM 333

RESULT 12
S63281
probable membrane protein YNL305c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein N0405
C:Species: Saccharomyces cerevisiae
C:Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 19-Apr-2002
A:Accession: S63281
A:Residues: 1-297 <MAU>
A:Experimental source: strain 5288C
A:Title: Sequence analysis of a 30 kb DNA segment from yeast chromosome XIV carrying a
C: and a novel putative serine/threonine protein kinase gene.
A:Reference number: S60394; MUID:96132033; PMID:8553702
A:Accession: S60395
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-297, 'D' <MAW>
A:Cross-references: EMBL:U23084
R:Maurer, K.T.C.
Submitted to the EMBL Data Library, March 1995
A:Reference number: S66127
A:Accession: S66127
A:Molecule type: DNA
A:Residues: 1-297 <MAP>
A:Cross-references: EMBL:U23084; NID:G1050853; PID:G1050855
C:Genetics:
A:Map position: 14L
C:Keywords: transmembrane protein
F:86-102/Domain: transmembrane #status predicted <TM1>
F:173-189/Domain: transmembrane #status predicted <TM2>
F:212-228/Domain: transmembrane #status predicted <TM3>
F:238-254/Domain: transmembrane #status predicted <TM4>
F:271-287/Domain: transmembrane #status predicted <TM5>

Query Match 11.2%; Score 143; DB 2; Length 297;
Best Local Similarity 24.3%; Pred. No. 1.7e-05;
Matches 65; Conservative 44; Mismatches 83; Indels 76; Gaps 13;

QY 31 PLV-OTHLKQVYLTCCALVASAAGAY-----LHI-LWNIGLLTTMACWGS 75
Db 44 PIIRQPMKHYKLSLSCQLLASLFCYVASTSLQNFIMSHIALFICVMVSLVSC--- 100
QY 76 MWLLSAP-----PYEQKR-----VALMAAALFEGA 103
Db 101 -IWLAVSPRPDEYASVPBLLTGSSEPAQQRPLPWYLSYKQKLTLLSIPTLSEAY 159
QY 104 SIGPIELGINPDSIVGAFVGCVAVFCESAAMLARREYLYLGLLSSGVSLFLWL 163
Db 160 CLS-LVTLA--YDKDTVLSALITTVVGVSLTALSER-----FENVLSATSIIYWL 210
QY 164 HF-----ASSIFGSGMAVFKFELYFGLL---VPVGIVFDTOEIEKAHLGDMDY 210
Db 211 NWGLTWIMCGMTALLFGWNTHSSKNFLYGLWGLALTAVLFDITDQLIFRKVY--PDEE 268
QY 211 VKHALTLFTDFGAVFVRILIMLNKXASE 238
Db 269 VRCAWMYLDIDVNLFLSILRI--LANSND 295

RESULT 13
AE3484
integral membrane protein [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
A:Accession: AE3484
R:Delvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes,
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella meliter
A:Reference number: AD3252; PMID:11756688
A:Accession: AE3484
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-245 <KUR>
A:Cross-references: GB:AE008917; PIDN:AAL53040.1; PID:G17983899; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:
A:Gene: EMBL1859
A:Map position: I
C:Superfamily: Escherichia coli ybhL protein

Query Match 10.7%; Score 136.5; DB 2; Length 245;
Best Local Similarity 29.1%; Pred. No. 5.3e-05;
Matches 64; Conservative 31; Mismatches 76; Indels 49; Gaps 10;

QY 55 AYHLILWN---IGGLTTMACMSMWLLSAPPYQ3-----QKRVALLMA--AALF---- 100
Db 29 SYMLGVYNNMAIGLAVTGLAAGFTAVLAQSNPAFQQLLFASPLRWVIMLAPLAAVFLSF 88
QY 101 -EGASIG-----PIELGINPDSIVGAFVGCVAVFCESAAMLARREYLY 148
Db 89 RIQSLSVGTACAIFWGYAALVGLSL-----SSIFVTGQSIIVTFFVTAASFGALSLEY 144
QY 149 -----LGLLSSGVSLFLWLHPAS--SIFGSMVAFKELYFGLLVFVGIVFDTOE 198
Db 145 TTKRNLSANGSFLMWG--LFGILASVNVNIFLGSTALQFAISVIGVLFAGLTAYDQOE 201
QY 199 IIEKAHLGD-----MDYVVKHALTFTDFGAVFVRILIM 232
Db 202 IKEMYEGDAADTQGRKIVNGALRLYLDLFINMFELQFM 241

RESULT 14
EB1729
conserved hypothetical protein TC0206 [imported] - Chlamydia muridarum (strain Nigg)
C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Sep-2000
A:Accession: EB1729
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: AB1500; MUID:20150255; PMID:10684935
A:Accession: EB1729
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-238 <TET>
A:Cross-references: GB:AE002287; GB:AE002160; NID:G17190237; PIDN:AAF39078.1; PID:G7190;
A:Experimental source: strain Nigg (MoPn)
C:Genetics:
A:Gene: TC0206
C:Superfamily: Escherichia coli ybhL protein

Query Match 10.3%; Score 130.5; DB 2; Length 238;
Best Local Similarity 27.2%; Pred. No. 0.00018;
Matches 66; Conservative 35; Mismatches 95; Indels 47; Gaps 12;

QY 20 YDSLKNYFQISPLVQTHLKQVY-----LTLCCALVASAAGAY--LHLWNIGLLTT 69
Db 4 YD--RDYTDQSRLPFTSSRVYGMWMTAGLAVTALTSGLYATGAYTFLSLW----WVWC 57
```

Search completed: May 25, 2003, 12:23:46
Job time : 44 secs

GenCore version 5.1.5
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OM protein - protein search, using sw model

Run on: May 25, 2003, 11:26:54 ; Search time 36 seconds
(without alignments)
285.726 Million cell updates/sec

Title: US-09-955-526-4

Perfect score: 1272

Sequence: 1 MEGTFFDQSASRNWSY.....LIIMLNASEKEKKKKERN 248

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1023.5	80.5	247	1 BIL_ARATH	Q91d45 arabidopsis
2	876.5	68.9	249	1 BIL_ORISA	Q9mbd8 oryza sativ
3	481.5	37.9	237	1 BIL_HUMAN	P55061 homo sapien
4	481.5	37.9	237	1 BIL_PAROL	Q91a79 paralichthy
5	479	37.7	236	1 BIL_RAT	P55062 rattus norv
6	312	24.5	245	1 BIL_DROME	Q9vsh3 drosophila
7	165	13.0	345	1 GHIT_HUMAN	Q9h3k2 homo sapien
8	157.5	12.4	219	1 YCCA_ECOLI	P08967 escherichia
9	143	11.2	237	1 YN45_YEAST	P48558 saccharomyc
10	130.5	10.3	238	1 Y206_CHLMU	Q9plal chlamydia m
11	128.5	10.1	238	1 Y819_CHLTR	O84826 chlamydia t
12	125.5	9.9	220	1 Y402_FASMU	Q9cnm5 pasteurella
13	124	9.7	231	1 Y893_DRIRA	Q9rvx8 deinococcus
14	123.5	9.7	231	1 Y236_CAMJE	Q9piq8 campylobact
15	122	9.6	234	1 YBHL_ECOLI	P75768 escherichia
16	121.5	9.6	232	1 YBHL_ECOLI	P09723 human cycop
17	120	9.4	222	1 YQ04_PSEAE	Q03268 pseudomonas
18	120	9.4	238	1 ZPRO_MOUSE	Q9da39 mus musculu
19	120	9.4	422	1 YF21_METJA	Q58916 methanococc
20	114.5	9.0	220	1 YCCA_HABIN	P44477 haemophilus
21	114	9.0	227	1 Y420_NEIMA	Q9jri0 neisseria m
22	113	8.9	223	1 YD58_VIBCH	Q9ksal vibrio chol
23	112.5	8.4	230	1 Y920_HELPY	Q25578 helicobacte
24	111	8.7	238	1 ZPRO_HUMAN	Q9hc24 homo sapien
25	109.5	8.6	230	1 Y920_HELPY	Q9zkt1 helicobacte
26	108.5	8.5	236	1 Y147_RICPR	Q9zel5 rickettsia
27	97	7.6	545	1 HGTL_CANAL	Q97611 candida alb
28	95	7.5	462	1 NHAC_BACFI	P27611 bacillus fi
29	93.5	7.4	630	1 S6A4_CAVPO	Q35899 cavia porce
30	93	7.3	234	1 YRUE_LACLA	Q9ceub lactococcus
31	92.5	7.3	229	1 Y358_STRPY	Q9alb9 streptococ
32	91	7.2	1124	1 TRPL_DROME	P48994 drosophila
33	90	7.1	1094	1 EMBA_MYCTU	P72060 mycobacteri

RESULT 1

ID	BIL_ARATH	STANDARD	PRT	247 AA
AC	Q9LD45			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Bax inhibitor-1 (BI-1) (AtBI-1).			
GN	BI-1 OR AT5G47120 OR K14A3.7.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsids.			
OX	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia;			
RX	MEDLINE=20086876; PubMed=10618494;			
RA	Kawai M., Pan L., Reed J.C., Uchimiya H.;			
RT	"Evolutionally conserved plant homologue of the Bax inhibitor-1 (BI-1)			
RT	gene capable of suppressing Bax-induced cell death in yeast.";			
REBS	Letts. 464:143-147(1999).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=cv. Columbia; TISSUE=Leaf;			
RC	MEDLINE=2024035; PubMed=10758491;			
RA	Sanchez P., de Torres Zabala M., Grant M.;			
RT	"AtBI-1, a plant homologue of Bax inhibitor-1, suppresses Bax-induced			
RT	cell death in yeast and is rapidly upregulated during wounding and			
RT	pathogen challenge.";			
RL	Plant J. 21:393-399(2000).			
RL	[3]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=cv. Columbia;			
RC	Kaneko T., Katch T., Asamizu E., Sato S., Nakamura Y., Kotani H.,			
RA	Tabata S.;			
RT	"Structural analysis of Arabidopsis thaliana chromosome 5. XI.";			
RT	Submitted (APR-1999) to the EMBL/Genbank/DBJ databases.			
CC	-1- FUNCTION: SUPPRESSOR OF APOPTOSIS.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).			
CC	-1- SIMILARITY: BELONGS TO THE BIL FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	-----			
CC	EMBL; A3025927; BAA98541.2; --			
DR	EMBL; AF208124; AAG35727.1; --			
DR	EMBL; AB025609; BAA98107.1; --			
DR	InterPro; IPR002199; Bax_inhbt1.			
DR	Pfam; PF01027; UPF0005; 1.			
DR	PROSITE; PS01243; B11; 1.			

Q9a2a3 caulobacter
O47479 loligo blee
Q9cdm7 lactococcus
O29470 archaeoglob
Q9evn4 pseudomonas
O51489 borrelia bu
P47562 mycoplasma
P28008 staphylococ
Q95919 polyporus
P13845 pseudomonas
P45064 haemophilus
Q18864 caenorhabdi

KW Apoptosis; Transmembrane. 80.5%; Score 1023.5; DB 1; Length 247;
 FT TRANSMEM 58 78 POTENTIAL.
 FT TRANSMEM 92 112 POTENTIAL.
 FT TRANSMEM 118 138 POTENTIAL.
 FT TRANSMEM 145 165 POTENTIAL.
 FT TRANSMEM 173 193 POTENTIAL.
 FT TRANSMEM 212 232 POTENTIAL.
 SQ SEQUENCE 247 AA; 27483 MW; FD3AAEA713363945 CRC64;

Query Match 80.5%; Score 1023.5; DB 1; Length 247;
 Best Local Similarity 77.4%; Pred. No. 1.3e-69;
 Matches 192; Conservative 31; Mismatches 24; Indels 1; Gaps 1;

QY 1 MEGTFFSFSQASRNKWSYDSLNKFRQISPLVQTHLKQVYLTCCALVASAAGAYLHL 60
 DB 1 MDAFSFFSFSQASRNKWSYDSLNKFRQISPLVQTHLKQVYLTCCALVASAAGAYLHL 59

QY 61 WNTGGLTTMACMGSMWLLSAPPYQEKRVALLMAALFEGASIGPIELGINDPSIV 120
 DB 60 WNTGGLTTGCGTGMWLLSAPPYQEKRVALLMAALFEGASIGPIELGINDPSIV 119

QY 121 FGAFVGCACVFCGSAAMLARREYLYLGLSSGVSLFWLHFASSIFGGSMAVFKFE 180
 DB 120 ITAFVGTATAFVCFSAAMLARREYLYLGLSSGVSLFWLHFASSIFGGSMAVFKFE 179

QY 181 LYFGLLVFGYIVFDTQBIIEKAHLGDMYVVKHALTLFTDFGAVFVRILIIIMLNASEKE 240
 DB 180 LYFGLLVFGYIVFDTQBIIEKAHLGDMYVVKHALTLFTDFGAVFVRILIIIMLNASEKE 239

QY 241 EKKKKRN 248
 DB 240 EKKKKRN 247

RESULT 2
 BIL ORYSA STANDARD; PRT; 249 AA.
 AC Q9MBD8,
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Bax inhibitor-1 (BI-1) (OsBI-1).
 GN BIL.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Yamahoushi;
 RX MEDLINE=20086876; PubMed=10618494;
 RA Kawai M., Pan L., Reed J.C., Uchimiya H.;
 RT "Evolutionally conserved plant homologue of the Bax inhibitor-1 (BI-1) gene capable of suppressing Bax-induced cell death in yeast."
 RL FEBS Lett. 464:143-147(1999).
 CC -!- FUNCTION: SUPPRESSOR OF APOPTOSIS (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: UBUIQUITOUS.
 CC -!- SIMILARITY: BELONGS TO THE BIL FAMILY.

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 CC -----
 DR EMBL; AB025926; BAA89540.3; -
 DR InterPro; IPR002139; Bax_inh1.
 DR Pfam; PF01027; UPF0005; 1.
 DR PROSITE; PS01243; BIL; 1.

KW Apoptosis; Transmembrane.
 FT TRANSMEM 39 59 POTENTIAL.
 FT TRANSMEM 65 85 POTENTIAL.
 FT TRANSMEM 93 113 POTENTIAL.
 FT TRANSMEM 119 139 POTENTIAL.
 FT TRANSMEM 151 171 POTENTIAL.
 FT TRANSMEM 213 233 POTENTIAL.
 SQ SEQUENCE 249 AA; 27114 MW; FEA3334173P6D384 CRC64;

Query Match 68.9%; Score 876.5; DB 1; Length 249;
 Best Local Similarity 66.3%; Pred. No. 1.1e-58;
 Matches 165; Conservative 40; Mismatches 43; Indels 1; Gaps 1;

QY 1 MEGTFFSFSQASRNKWSYDSLNKFRQISPLVQTHLKQVYLTCCALVASAAGAYLHL 60
 DB 1 MDAFSFFSFSQASRNKWSYDSLNKFRQISPLVQTHLKQVYLTCCALVASAAGAYLHL 60

QY 61 WNTGGLTTMACMGSMWLLSAPPYQEKRVALLMAALFEGASIGPIELGINDPSIV 120
 DB 61 WNTGGLTTMACMGSMWLLSAPPYQEKRVALLMAALFEGASIGPIELGINDPSIV 120

QY 121 FGAFVGCACVFCGSAAMLARREYLYLGLSSGVSLFWLHFASSIFGGSMAVFKFE 180
 DB 120 ITAFVGTATAFVCFSAAMLARREYLYLGLSSGVSLFWLHFASSIFGGSMAVFKFE 180

QY 181 LYFGLLVFGYIVFDTQBIIEKAHLGDMYVVKHALTLFTDFGAVFVRILIIIMLNASEK- 239
 DB 181 LYFGLLVFGYIVFDTQBIIEKAHLGDMYVVKHALTLFTDFGAVFVRILIIIMLNASEK- 240

QY 240 EKKKKRN 248
 DB 241 EKKKKRN 249

RESULT 3
 BIL HUMAN STANDARD; PRT; 237 AA.
 AC P55061; O14938; Q96J50.
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Bax inhibitor-1 (BI-1) (Testis enhanced gene transcript).
 GN BIL OR TEST.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=96015061; PubMed=8530040;
 RA Walter L., Marynen P., Szpirer J., Levan G., Guenther E.;
 RT "Identification of a novel conserved human gene, TEST."
 RL Genomics 28:301-304(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Cowling R.T., Birnboim H.C.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Strausberg R.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE=98325348; PubMed=9660918;
 RA Xu Q., Reed J.C.;
 RT "Bax inhibitor-1, a mammalian apoptosis suppressor identified by functional screening in yeast."
 RL Mol. Biol. Cell 1:337-346(1998).
 CC -!- FUNCTION: SUPPRESSOR OF APOPTOSIS.
 CC -!- SUBUNIT: INTERACTS WITH BCL2 AND BCL-XL.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

```

CC -!- TISSUE SPECIFICITY: HIGHLY ABUNDANT IN TESTIS.
CC -!- SIMILARITY: BELONGS TO THE B11 FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; X75861; CAA53472.1; -.
CC DR EMBL; AF033095; AAB87479.1; -.
CC DR EMBL; BC000916; AAH00916.1; -.
CC DR Genew; HGNC:11723; REG1.
CC DR MIM; 600748; -.
CC DR InterPro; IPR002199; Bax_inhbt1.
CC DR Pfam; PF01027; UPOF005; 1.
CC DR PROSITE; PS01243; B11; 1.
CC DR Apoptosis; Transmembrane.
CC KW TRANSMEM 30 50
CC FT TRANSMEM 53 73
CC FT TRANSMEM 87 107
CC FT TRANSMEM 113 133
CC FT TRANSMEM 140 160
CC FT TRANSMEM 167 187
CC FT TRANSMEM 207 227
CC FT TRANSMEM 269 269
CC FT CONFLICT 169 169
CC FT CONFLICT 187 187
CC FT CONFLICT 187 187
CC SQ SEQUENCE 237 AA; 26537 MW; 6567E73A1AD6238E CRC64;
CC -----
Query Match 37.9%; Score 481.5; DB 1; Length 237;
Best Local Similarity 42.7%; Pred. No. 2.7e-29;
Matches 99; Conservative 52; Mismatches 74; Indels 7; Gaps 4;
CC -----
QY 19 SYDSLKNVQIQLSPVQTHLKQVYLTLCCALVASAGAYLHILWNI--GGLLTMACMGSM 76
DB 9 NFDALLKFSHITFTSQOHLKKVYAFALCMFAAAGAYVHMVTHFQAGLLSALGSLIM 68
QY 77 VLLSLAPPYQ--EQKRVALLMAALFEAGISGLTELGINFDPISVFGAVGCVFGCF 134
DB 69 IWLWATPHSHETQKELGLLAGFAFLTGVLGPALEFCIAVNPISILTPAMGTAMIFTCP 128
QY 135 SAAMALARREYLYLGGLLSGCVSLLFWLHPASSIFGGSMAVFKFLYPLGLVFGVYIVF 194
DB 129 TLSALYARRSRSLFTGGILMGALSILL--LSSLGNVFFGSIWLFQANLYVGLVVMCGFVLF 187
QY 195 DTQEIIEKAHLGDMDVYKHALFTFDGCAVFRILITMLKNASKEKEKKR 246
DB 188 DTQLIIEKAHGDDQYVHNCIDFLDFITVFRKUMMILAWN--EKDKKKEK 237
CC -----
RESULT 4
B11_PAROL
ID B11 PAROL STANDARD; PRT; 237 AA.
AC Q2IA79;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, last sequence update)
DT 16-OCT-2001 (Rel. 40, last annotation update)
DE Probable Bax inhibitor-1 (B1-1).
OS Paralicthys olivaceus (flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Paralicthidae; Paralicthys.
OC NCBI_TaxId=8255;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Lee J., Jeon J., Song Y.;
RT "Liver cDNA from Japanese flounder with similarity to TEGT.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: SUPPRESSOR OF APOPTOSIS (BY SIMILARITY).

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CC CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC CC -!- TISSUE SPECIFICITY: HIGHLY ABUNDANT IN TESTIS.
CC CC -!- SIMILARITY: BELONGS TO THE B11 FAMILY.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL: AF220548; AAF61067.1; -.
CC CC InterPro: IPR002199; Bax_inhbt1.
CC CC Pfam: PF01027; UPF0005; 1.
CC CC PROSITE: PS01243; B11; 1.
CC CC KW Apoptosis; Transmembrane.
CC CC FT TRANSMEM 30 50 POTENTIAL.
CC CC FT TRANSMEM 53 73 POTENTIAL.
CC CC FT TRANSMEM 87 107 POTENTIAL.
CC CC FT TRANSMEM 113 133 POTENTIAL.
CC CC FT TRANSMEM 150 170 POTENTIAL.
CC CC FT TRANSMEM 173 193 POTENTIAL.
CC CC SQ SEQUENCE 237 AA; 26570 MW; 344181AA386AB9A6 CRC64;
CC CC -----
CC CC Query Match 37.9%; Score 481.5; DB 1; Length 237;
CC CC Best Local Similarity 41.3%; Pred. No. 2.7e-29;
CC CC Matches 95; Conservative 53; Mismatches 77; Indels 5; Gaps 3;
CC CC -----
CC CC QY 19 SYDSLKNFRQISPLVQTHLKQVYLTCCALVSAAGAYLHLWNI--GGLLTTMACMGSM 76
CC CC :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
CC CC Db 9 NFDSLKFQSIQSHSTQVHLKNVYSSLVACMFVAAGSYVHVVTRLFQGGMLSVLGSGLWM 68
CC CC QY 77 VMLISAP--PYEQQRVALLMAALFGASIGPLIELGNFDESIVFGAFVGCADVFGCF 134
CC CC :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
CC CC Db 69 FLWMTPEHNSETEKRLAILAGFAFLVGLVGLCTPLDFVAINESIIVTFLGTSVIFVCF 128
CC CC QY 135 SAAAMLARRELYLGGLLSGVSLFLWLFHFASSIFGGSMVAFKFLYELGLLVFGYIVF 194
CC CC :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
CC CC Db 129 TLSALYAKERSYFLGGTLMGSLFILMSWMNFF--GSVNLFFKAHWLGLLLIMCGVLX 187
CC CC QY 195 DTCEIIEKAHLGDMYVKAHLTLTDFCAVFRVILLIMLKNASEKEKKK 244
CC CC :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
CC CC Db 188 DTQLIIEKAENGDKDYVWHVSVDLFDFTIFRKLWVILALNDKKKKKK 237
CC CC -----
CC CC RESULT 5
CC CC BIL_RAT
CC CC ID BIL_RAT STANDARD; PRT; 236 AA.
CC CC AC F55062; Q64712;
CC CC DT 01-OCT-1996 (Rel. 34, Created)
CC CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
CC CC DE 16-OCT-2001 (Rel. 40, Last annotation update)
CC CC DE Bax inhibitor-1 (BI-1) (Testis enhanced gene transcript).
CC CC GN B11 OR TEST.
CC CC OS Rattus norvegicus (Rat).
CC CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CC CC NCBI_TaxId=10116;
CC CC [1]
CC CC SEQUENCE FROM N.A.
CC CC RC STRAIN=Sprague-Dawley; TISSUE=Testis;
CC CC EX MEDLINE=94281747; PubMed=801211;
CC CC RA Walter L., Dirks B., Rothermel E., Heyens M., Szpirer C., Levan G.,
CC CC RA Guenther E.;
CC CC RA RT "A novel, conserved gene of the rat that is developmentally regulated
CC CC in the testis.";
CC CC RL Mamm. Genome 5:216-221(1994).
CC CC -!- FUNCTION: SUPPRESSOR OF APOPTOSIS (BY SIMILARITY).
CC CC -!- SUBUNIT: INTERACTS WITH BLC2 AND BCL-XL (BY SIMILARITY).
CC CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC CC -!- TISSUE SPECIFICITY: HIGHLY ABUNDANT IN TESTIS.
CC CC -!- SIMILARITY: BELONGS TO THE B11 FAMILY.

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Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
de Palcos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodon K.J., Evangelista C.C., Ferraz C., Ferreira S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Gelbart W.M., Fleisschmann W.,
Foster C., Gabrielian A.B., Garg N.Z., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jajali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McJueod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
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-!- FUNCTION: SUPPRESSOR OF APOPTOSIS (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE BIL FAMILY.
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Query Match 24.58; Score 312; DB 1; Length 245;
Best Local Similarity 34.4; Pred. No. 1.2e-18;
Matches 77; Conservative 48; Mismatches 83; Indels 16; Gaps 5

QY 31 PLVQTHLKQVYLTCALVASAAGAYLHI--LWNIGGLLTMTACMSWYLLSAPPYQEQ 88
Db 25 PYVREHLSKYVWLGSTAAATAMGAMQLMRDFLDLG---VLAAVATLVLLGLHFHYKDD 80
QY 89 -----KVALLMAAALPGASIGPLIELGINFDPDSIVFGAVFCVAVGFCFSAAMLAR 143
Db 81 GKNYITRIGMLYAFGFCGGQTLGELLGVICINPAILISALTGTFTVFTLSLSALLAEQ 140
QY 144 REYLYLGLLSGVSLLEFWLHFASSIFGGSNAVEKFLYELGLLVFGYIVFDQETIEKA 203
Db 141 GKLYLGGMLVSVINTALLSLFNWVF-KSYFVQVQTLVYGVFVMAAFIVYDQNIIVEK 199
QY 204 HLGDDMDYKHALTFTDFGAVFVILIMLKVASEKEEKKKR 247
Db 200 RGNRDVVGHAULDFDLVLSFRLLIL-----FQKEKRQNER 239

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RESULT 7
 CHIT_HUMAN STANDARD; PRT; 345 AA.
 AC Q9H3K2; O95894; Q9H0P2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Growth hormone inducible transmembrane protein (Dermal papilla derived protein 2) (Myo21 protein) (F0D010).
 DE GH1TM OR DERP2.
 CN HOMO sapiens (Human).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Dermal papilla;
 RA Ikeda A., Yamashita M., Yoshimoto M.;
 RT "Molecular cloning of a dermal papilla derived gene.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Mei G., Yu W., Gibbs R.A.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Mao Y.M., Xie Y., Mu Z.M., Li Y., Huang Y.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=21154917; PubMed=11230166;
 RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
 RA Ansgore W., Boecker M., Bloeker H., Bauersachs S., Blum H.,
 RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
 RA Meves H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
 RA Wambutt R., Korn B., Klein M., Poustka A.;
 RT "Towards a catalog of human genes and proteins: sequencing and
 RT analysis of 500 novel complete protein coding human cDNAs.";
 RL Genome Res. 11:422-435 (2001).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Urinary bladder;
 RA Strauberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- SIMILARITY: BELONGS TO THE BII FAMILY.
 CC -----
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 CC -----
 DR EMBL; AB009685; BAA3049.1; -
 DR EMBL; AF131820; AAD20052.1; -
 DR EMBL; AF060923; AAG43135.1; -
 DR EMBL; AL136713; CAB66648.1; -
 DR EMBL; BC010354; AAH10354.1; -
 DR Genew; HGNC:17281; GH1TM.
 DR InterPro; IPR002199; Bax_inhbt1.
 DR Pfam; PF01027; UPF0005; 1.
 KW Transmembrane.
 FT TRANSMEM 83 103 POTENTIAL.
 FT TRANSMEM 126 146 POTENTIAL.
 FT TRANSMEM 160 180 POTENTIAL.
 FT TRANSMEM 191 211 POTENTIAL.
 FT TRANSMEM 214 234 POTENTIAL.

FT TRANSMEM 245 265 POTENTIAL.
 FT TRANSMEM 272 292 POTENTIAL.
 FT CONFLICT 4 4 A -> V (IN REF. 4).
 FT CONFLICT 64 64 E -> G (IN REF. 3).
 FT CONFLICT 74 74 I -> M (IN REF. 4).
 FT CONFLICT 118 118 Q -> R (IN REF. 4).
 SQ SEQUENCE 345 AA; 37205 MW; 809FAED86A9CD98E CRC64;
 Query Match 13.0%; Score 165; DB 1; Length 345;
 Best Local Similarity 26.3%; Pred. No. 1.4e-05;
 Matches 61; Conservative 47; Mismatches 86; Indels 38; Gaps 11;
 QY 36 HLKQVYITLCCALVASAGAYLH--ILWNI---GGLLT---TWACMGSMVWLLSAPPYQE 87
 DB 125 HSTYITLAGSIGTALSIAISRTPLVLMFMFMVGRGVTIGVTPFAAMVGAGMLVRSIPYDQ 184
 QY 88 Q---KRVALLMAALFEGASIGPLIELGINFDFSVFGCAVVGCAVFGCFSAAAMLARR 144
 DB 185 SPGPKHLAWLLHSGVM-GAVVAPLTILG---GELLIRAAWYTAGIV-GGLSTVAMCAPSE 239
 QY 145 EYVLGGLSSGVSLFLWLFHFASSIFGGM-----AVFKFELYGLLVFGYIVF 194
 DB 240 KFLNMGAPLGVGLGV-----FVSSL--GSMFLPPTTVAGATILYSVAMYGGLVLFNSFLY 293
 QY 195 DTQBIIEKAHLGDM-----DYVKHALTLTDFGAVFVRLIIMLKNASEKE 240
 DB 294 DTQKVIKRAVSPMYGVQKYDPINSLMSIYMDTLNIFMRVATMLATGGNRKK 345
 RESULT 8
 YCCA_ECOLI STANDARD; PRT; 219 AA.
 ID YCCA_ECOLI
 AC P06957;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein ycca.
 GN YCCA OR B0970.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia
 OC Escherichia
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84236106; PubMed=6376117;
 RA Tamura F., Nishimura S., Ohki M.;
 RT "The E. coli dive mutation, which differentially inhibits synthesis
 RT of certain proteins, is in TENASE1";
 RL EMBO J. 3:1103-1107 (1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474 (1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97061202; PubMed=8905232;
 RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
 RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
 RA Yano M., Horiuchi T.;
 RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 12.7-28.0 min region on the linkage map.";
 RL DNA Res. 3:137-155 (1996).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RT Eisen J., Fraser C.M.;
RL "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
pneumoniae A539";
RL Nucleic Acids Res. 28:1397-1406(2000).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE BIL FAMILY.
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CC
CC EMBL; AE002287; AAF39078.1; -;
DR TIGR; TC0206; -;
DR InterPro; IPR002199; Bax inhbr1.
DR Pfam; PF01027; UPF0005; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 22 42 POTENTIAL.
FT TRANSMEM 49 69 POTENTIAL.
FT TRANSMEM 78 98 POTENTIAL.
FT TRANSMEM 105 125 POTENTIAL.
FT TRANSMEM 141 161 POTENTIAL.
FT TRANSMEM 166 186 POTENTIAL.
FT TRANSMEM 208 228 POTENTIAL.
FT TRANSMEM 238 258 POTENTIAL.
SQ SEQUENCE 238 AA; 26309 MW; 4625B1D88093657E CRC64;
Query Match 10.3%; Score 130.5; DB 1; Length 238;
Best Local Similarity 27.2%; Pred. No. 0.0037;
Matches 66; Conservative 35; Mismatches 95; Indels 47; Gaps 12;
QY 20 YDLSKNFRQISPLVQTHLKQVY-----ITLCCALVASAAGAY--LHLWNIGGLTT 69
DB 4 YD--RDYQDSRLPGTSSRYGWNVTAGLAVTALTSGLYATGAYRTLSLW----WVWC 57
QY 70 MACMG-----SMWLLSAPPYQKQKRVALLMAALFEGASIGPLIEL-GINFDPPIVFG 122
DB 58 FATLGVSFYIOAQIKLSVPAV-----MGLFLAYSVLGEMFFGTMVPYAAQFGGIVWA 112
QY 123 AFVGCNAVFGCFSAAAMLAR-----RREYVIGGLSSGVSLLFWLHPASSIFGGSMA 175
DB 113 AFGSAVIFGLSAAAGFTKSDLTQIHRILMALIGLWV--ISLGF---LVVSLFTMPL 167
QY 176 VKFELYFGLLVFGYIVFDTCETIEKAHL-----GDMDY---VKHALTLFTDFGAVFVRI 228
DB 168 MLLCYLGLIIFVGLTVVDAQSIRRVARSVGDHGLDLSYKLSLIMALQMYCNVIMIFWYL 227
QY 229 LII 231
DB 228 LQI 230
RESULT 11
Y819 CHLTR
ID Y819 CHLTR STANDARD; PRT; 238 AA.
AC O84826;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein CT819.
GN CT819.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/UN-3/Cx;
RX MEDLINE=99000809; PubMed=9784136;
RA Stephens R.S., Kaiman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,

RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
Chlamydia trachomatis";
RL Science 282:754-759(1998).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE BIL FAMILY.
CC
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CC
CC EMBL; AE001354; AAC68416.1; -;
DR InterPro; IPR002199; Bax inhbr1.
DR Pfam; PF01027; UPF0005; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 22 42 POTENTIAL.
FT TRANSMEM 49 69 POTENTIAL.
FT TRANSMEM 78 98 POTENTIAL.
FT TRANSMEM 105 125 POTENTIAL.
FT TRANSMEM 141 161 POTENTIAL.
FT TRANSMEM 166 186 POTENTIAL.
FT TRANSMEM 208 228 POTENTIAL.
FT TRANSMEM 238 258 POTENTIAL.
SQ SEQUENCE 238 AA; 26264 MW; FD101F7B3867B8E5 CRC64;
Query Match 10.1%; Score 128.5; DB 1; Length 238;
Best Local Similarity 25.9%; Pred. No. 0.0052;
Matches 63; Conservative 38; Mismatches 95; Indels 47; Gaps 12;
QY 20 YDLSKNFRQISPLVQTHLKQVY-----LTLCCALVASAAGAY--LHLWNIGGLTT 69
DB 4 YD--RDYQDSRLPGTSSRYGWNVTAGLAVTALTSGLYATGAYRTLSLW----WVWC 57
QY 70 MACMG-----SMWLLSAPPYQKQKRVALLMAALFEGASIGPLIEL-GINFDPPIVFG 122
DB 58 FATLGVSFYIOAQIKLSVPAV-----MGLFLAYSVLGEMFFGTMVPYAAQFGGIVWA 112
QY 123 AFVGCNAVFGCFSAAAMLAR-----RREYVIGGLSSGVSLLFWLHPASSIFGGSMA 175
DB 113 AFGSAVIFGLSAAAGFTKSDLTQIHRILMALIGLWV--ISLGF---LVVSLFTMPL 167
QY 176 VKFELYFGLLVFGYIVFDTCETIEKAHL-----GDMDY---VKHALTLFTDFGAVFVRI 228
DB 168 LYLCCYLGLIIFVGLTVVDAQSIRRVARSVGDHGLDLSYKLSLIMALQMYCNVIMIFWYL 227
QY 229 LII 231
DB 228 LQI 230
RESULT 12
Y402 PASMU
ID Y402 PASMU STANDARD; PRT; 220 AA.
AC Q9CWN5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein PM0402.
GN PM0402.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PM70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RA "Complete genomic sequence of Pasteurella multocida PM70";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

```

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE B11 FAMILY.
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CC -----
CC EMBL; AB060676; AAK02486.1; -
CC InterPro: IPR002199; Bax_inhbt1.
CC Pfam: PF01027; UPF0005; I.
CC Hypothetical protein; Transmembrane; Complete proteome.
CC TRANSMEM 25 45 POTENTIAL.
CC TRANSMEM 50 70 POTENTIAL.
CC TRANSMEM 74 94 POTENTIAL.
CC TRANSMEM 105 125 POTENTIAL.
CC TRANSMEM 135 155 POTENTIAL.
CC TRANSMEM 158 178 POTENTIAL.
CC TRANSMEM 195 216 POTENTIAL.
CC TRANSMEM 220 AA; 23936 MW; 8EEC2E3FB4B5CDD5 CRC64;
CC SEQUENCE
CC -----
Query Match 9.9%; Score 125.5; DB 1; Length 220;
Best Local Similarity 25.4%; Pred. No. 0.0081;
Matches 53; Conservative 44; Mismatches 93; Indels 19; Gaps 10;
QY 32 LVQTH-LKQVLTCCALVASAGAYLHILNI--GGILTTMACGSMWLLSAPPVQ- 86
DB 14 LKTHKVRNTYELGLTAFSAVAIYSMSLNLPRPGILMLAGFYGLLFL----TVKL 69
QY 87 EQKRVALLMAAL--PEGASIGLELBIQINFDPP-SIVFGAFVG-CAVVGFCFSMAAMLAR 142
DB 70 SNSGIGLISFTAFGTGLVGLVNVVSHGAGDIVLALAGTAAVFAC--GAYVLT 127
QY 143 RREYLYGLLLSGVLLFWLHFASISFGSMVAFKELYFGLLVFVGYVDFICEIEK 202
DB 128 KQMSFLSGTIFALFVLLGVMASFFQSPMLYTAISGLFVVFSTLGL-ILYETSNII-- 184
QY 203 AHLGDMDYVKHALTFTDFGAFVRLII 231
DB 185 -HGNETYIRATVSI FVSLYNLISLNI 212
RESULT 13
Y893 DEIRA STANDARD; PRT; 231 AA.
AC Q9RVX8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein DR0893.
GN DR0893.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RL;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1."
RL Science 286:1571-1577(1999).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

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CC -!- SIMILARITY: BELONGS TO THE B11 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB001942; AAF10471.1; -
CC TIGR; DR0893; -
CC InterPro: IPR002199; Bax_inhbt1.
CC Pfam: PF01027; UPF0005; I.
CC Hypothetical protein; Transmembrane; Complete proteome.
CC TRANSMEM 26 46 POTENTIAL.
CC TRANSMEM 56 76 POTENTIAL.
CC TRANSMEM 84 104 POTENTIAL.
CC TRANSMEM 112 132 POTENTIAL.
CC TRANSMEM 142 162 POTENTIAL.
CC TRANSMEM 163 183 POTENTIAL.
CC TRANSMEM 206 226 POTENTIAL.
CC SEQUENCE 231 AA; 24447 MW; BBB7D76A6445D9C9 CRC64;
CC -----
Query Match 9.7%; Score 124; DB 1; Length 231;
Best Local Similarity 26.2%; Pred. No. 0.011;
Matches 62; Conservative 41; Mismatches 94; Indels 40; Gaps 10;
QY 23 LKNPQISPLVQVTHLKQV-----YLTCCALVASAGAYL-----HILWNIGGL-LTT 69
DB 2 VASMQLIANTQKTLQDQVTFWARTYSMAAGLALTAGVAVLTAQNEGLAMQVASLRPL 61
QY 70 MACGSMWLLSAPPYQKRVALLMAALPEG-ASIGPLI--ELGINFDPISVFGAFVG 126
DB 62 MLAQLALVFVLS---MFAQRLSAAVAGALFVGVAULTGLTFSALLFAYSPPAAVITAFV 117
QY 127 CAVVGFCFSMAAMLAR-----REYLYGLLLSGVLLFWLHFASISFGSMVAFKFE 180
DB 118 SAGTGLMSVAGFVKIKDLSAMGRFFLE--AVLGLVAMLV-----NLFVGSALSIGI 169
QY 181 LYFGLLVFVGYVDFDTQIIEKAHLG-----DMDYVKHALTFTDFGAFVRLII 231
DB 170 SMIGVFLFAGLTAYDTQMLRNLLALSGISGEQASINGALALYLDIFINIFLNI 226
RESULT 14
Y236 CAMJE STANDARD; PRT; 231 AA.
AC Q9PIQ8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein Cj0236c.
GN Cj0236c.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 11168;
RX MEDLINE=20150312; PubMed=1068204;
RA Parkhill J., Wren B.W., Mungall K., Kettle J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences."
RL Nature 403:665-668(2000).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE B11 FAMILY.
CC -----

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CC or send an email to license@isb-sib.ch).

DR EMBL; AL139074; CAB72705.1; -
DR InterPro; IPR002199; Bax_inhbr1.
DR Pfam; PF01027; UPF0005; I.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 36 56 POTENTIAL.
FT TRANSMEM 58 78 POTENTIAL.
FT TRANSMEM 83 103 POTENTIAL.
FT TRANSMEM 143 163 POTENTIAL.
FT TRANSMEM 170 190 POTENTIAL.
SQ SEQUENCE 231 AA; 25487 MW; 279E67CA380336C9 CRC64;

Query Match 9.7%; Score 123.5; DB 1; Length 231;
Best Local Similarity 26.8%; Pred. No. 0.012;
Matches 62; Conservative 38; Mismatches 100; Indels 31; Gaps 10;
QY 20 YDSLKNFRQI-SPLVOTELKQVYLTLCCALVASAAGAYLHL-----WNIGLLTTWACMG 74
Db 8 YSRSEFENTRSELSIRIKQYQLFAASLLAATVGAVGIFALASPIQSQVTFWLFA 67
QY 75 SMVLLSAPPYQEQKRVALLMAALF-----EGASIGPLI--ELGINFDPISIVFGAFVC 127
Db 68 VBIGLLFA--LQMKREAPLNVLVLFGTFCGLTLPLLSVLAIPAGGIIIAQAFALT 125
QY 128 AVVFCGSAAMLRREVLVGG-----LSSGVSLFLWLFHFASSIFGSGMAVFKPELY 182
Db 126 TVAFAGLSVFAM-NTKKFTVTGKALFVLIVVAASLLNLFSSIVNLAISA----- 178
QY 183 FGLLVFGVIVDTQEIIEKAHLGDMY-VKHALTLTFDFGAVFVRILIM 232
Db 179 VAAILFSFYLYDTQNIIR---GNVETPIEGAVLYLDFVNLVLSLNL 225

RESULT 15

ID YBHL_ECOLI STANDARD; PR7; 234 AA.
AC P75768;
DT 15-JUL-1998 (Rev. 36, Created)
DT 15-JUL-1998 (Rev. 36, Last sequence update)
DT 16-OCT-2001 (Rev. 40, Last annotation update)
DE Hypothetical protein ybhl.
GN YBHL OR B0786.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.,
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikenoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saigo N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;

RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res 3:137-155 (1996).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE BIL FAMILY.

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DR EMBL; AE000181; AAC73873.1; -
DR EMBL; D90716; BAA35444.1; -
DR EcoGene; EGI3668; ybhl.
DR InterPro; IPR002199; Bax_inhbr1.
DR Pfam; PF01027; UPF0005; I.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 24 44 POTENTIAL.
FT TRANSMEM 57 77 POTENTIAL.
FT TRANSMEM 80 100 POTENTIAL.
FT TRANSMEM 103 123 POTENTIAL.
FT TRANSMEM 137 157 POTENTIAL.
FT TRANSMEM 164 184 POTENTIAL.
FT TRANSMEM 207 227 POTENTIAL.
SQ SEQUENCE 234 AA; 25902 MW; 7A59105563D5DFC8 CRC64;

Query Match 9.6%; Score 122; DB 1; Length 234;
Best Local Similarity 25.5%; Pred. No. 0.016;
Matches 59; Conservative 41; Mismatches 81; Indels 50; Gaps 11;
QY 33 VQTHLKQVY-----ITLCCALVASAAGAYLHLWN-----IGLLTTMA---CMGSM 76
Db 17 LQTYMAQYGYWMTVGLLITAFVAVYAANSAVMELLFTNRVFLIGLIIAQLALVIVLSAM 76
QY 77 VMLLSAPPYQEQKRVALLMAALFEGASIGPLIELGINFDPSIVFGAFVCAVFGCPSA 136
Db 77 IQKLSA-----GVTTMLFMYLSALTGLTSSIF---IVYTAASIASTFFVTAGMFGMSL 128
QY 137 AAMLARR-----REYLY---LGILLSGVSLFLWLFHFASSIFGSGMAVFKFELYFGLLYF 188
Db 129 YGYTTKRDLSGFGNMLFWALIGIVLASLVN--FWLK-----SEALMWAVTYIGVIVF 178
QY 189 VGYIVFDTOEII---EKHLGDMYVKH-----ALTLFTDFGAVFVRILII 231
Db 179 VGLTAYDTQKLNWGEQIDTRDTSNLRKYSILGALTLYLDFINLFLMLLRI 229

Search completed: May 25, 2003, 12:21:40
Job time : 39 secs

GenCore version 5.1.5
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OM protein - protein search, using sw model

Run on: May 25, 2003, 12:05:29 ; Search time 58 Seconds
(without alignments)
881.029 Million cell updates/sec

Title: US-09-955-526-4

Perfect score: 1272
Sequence: 1 MEGTSPFDSQASRNWSY.....LIIMLNASEKEKKKRRN 248

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 21:
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1134.5	89.2	249	10 Q93XB9	Q93XB9 nicotiana t
2	1010.5	79.4	247	10 Q93XC0	Q93XC0 brassica na
3	1002.5	78.8	246	10 Q8W196	Q8W196 brassica ol
4	883	69.4	247	10 Q93XL2	Q93XL2 hordeum vul
5	490.5	38.6	237	11 Q9D2C7	Q9D2C7 mus musculu
6	472	37.1	262	10 Q23599	Q23599 arabidopsis
7	435.5	34.2	187	10 Q9L7B6	Q9L7B6 arabidopsis
8	192	15.1	305	5 Q9VIB2	Q9VIB2 drosophila
9	192	15.1	365	5 Q8ZQ61	Q8ZQ61 drosophila
10	174.5	13.7	219	16 Q8T824	Q8T824 drosophila
11	172	13.5	341	5 Q9VZ34	Q9VZ34 drosophila
12	171	13.4	346	11 Q91VC9	Q91VC9 mus musculu
13	170.5	13.4	219	16 Q8Z7R5	Q8Z7R5 salmonella
14	164	12.9	99	6 Q95309	Q95309 sus.scrofa
15	157.5	12.4	219	16 Q8XD81	Q8XD81 escherichia
16	150	11.8	233	16 Q8Y034	Q8Y034 ralstonia s

17	144	11.3	266	3	O74888	O74888 schizosacch
18	143.5	11.3	342	5	P91373	P91373 caenorthabdi
19	141.5	11.1	237	12	O8V310	O8V310 camelbox vi
20	141.5	11.1	237	12	O8QO86	O8QO86 camelbox vi
21	136.5	10.7	245	16	O8YEL9	O8YEL9 brucella me
22	132	10.4	319	4	Q9Y6G2	Q9Y6G2 homo sapien
23	131.5	10.3	228	12	Q8QRT8	Q8QRT8 chimpanzee
24	128	10.1	236	16	Q8ZGM1	Q8ZGM1 yersinia pe
25	124.5	9.8	239	10	Q9M1V9	Q9M1V9 arabidopsis
26	123	9.7	316	5	Q9ST37	Q9ST37 drosophila
27	123	9.7	324	5	Q9V6H7	Q9V6H7 drosophila
28	122	9.6	234	16	O8X804	O8X804 escherichia
29	119	9.4	284	4	Q9HCL9	Q9HCL9 homo sapien
30	118.5	9.3	239	5	Q9V6H6	Q9V6H6 drosophila
31	117.5	9.2	245	16	Q9Z1L61	Q9Z1L61 rhizobium m
32	116	9.1	244	5	Q8T8W2	Q8T8W2 drosophila
33	113.5	8.9	229	10	Q94GN3	Q94GN3 oryza sativ
34	113	8.9	210	12	O72763	O72763 cowpox viru
35	112	8.8	232	16	Q8Z2Q4	Q8Z2Q4 salmonella
36	112	8.8	256	10	Q94A20	Q94A20 arabidopsis
37	111	8.7	232	16	Q8ZKW9	Q8ZKW9 agrobacteri
38	109	8.6	260	16	Q8UC16	Q8UC16 agrobacteri
39	109	8.6	311	4	Q869X1	Q869X1 homo sapien
40	109	8.6	311	4	Q8TAM3	Q8TAM3 homo sapien
41	108.5	8.5	1107	10	Q9ATP8	Q9ATP8 acetabulari
42	108.5	8.5	1112	10	Q9FNX2	Q9FNX2 acetabulari
43	106	8.3	234	16	Q8ZQP9	Q8ZQP9 salmonella
44	106	8.3	284	5	Q9VFM3	Q9VFM3 drosophila
45	106	8.3	659	16	Q8Y6E1	Q8Y6E1 listeria mo

ALIGNMENTS

RESULT 1

Q93XB9 ID Q93XB9 PRELIMINARY; PRT; 249 AA.
AC Q93XB9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Bax inhibitor 1.
GN Bi-1.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_taxid=4097;
RN [1]_taxid=4097;
RP SEQUENCE FROM N.A.
RC STRAIN=CV. SR-1; TISSUE=LEAF;
RA Boiduc N., Pitre F., Brisson L.;
RT "Characterization of Bax inhibitor 1 from Nicotiana tabacum."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF390556; AAK73102.1; -
DR InterPro; IPR002199; Bax_inhbt1.
DR InterPro; IPR001064; Crystallin.
DR Pfam; PF01027; UFF0005; 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN 1.
SQ SEQUENCE 249 AA; 27604 MW; 776ECC35BEFB9F8 CRC64;

Query Match 89.2%; Score 1134.5; DB 10; Length 249;

Best Local Similarity 87.1%; Pred. No. 5.7e-92;

Matches 217; Conservative 21; Mismatches 10; Indels 1; Gaps 1;

QY 1 MEGTSPFDSQSA-SRNWSYDSLKNFRQISPLVQTHLKQVYITLCCALVASAAGAYLHI 59

Db 1 MESCSTFFNSQSSASRNWSYDSLKNFRQISPLVQTHLKQVYITLCCALVASAAGAYLHI 60

QY 60 LWNIGLLTTHACGSMYVLLSAPPYQEQEVALMAALPEGASIGLPIELGINDPSI 119

Db 61 LWNIGLLTTHACGSMYVLLSAPPYQEQEVALMAALPEGASIGLPIELGINDPSI 120

```

QY 120 VFAGVGCVAVFCFSAAMARRRYLYLGLSSGVSLFLFWLHFASSIFGGSMAVFKF 179
Db 121 VIGAFVGCVAVFCFSAAMARRRYLYLGLSSGVSLFLFWLHFASSIFGGSMAVFKF 180
QY 180 ELYFGLLVFVGIVFTQETIEIKAHGDMYVVKHALTFTDFGAVFVRILIMLKNASEK 239
Db 181 EVYFGLLVFVGIVFTQETIEIKAHGDMYVVKHALTFTDFGAVFVRILIMLKNASEK 240
QY 240 EKKKKRRN 248
Db 241 EKKKKRRN 249

RESULT 2
Q93XC0 PRELIMINARY; PRT; 247 AA.
AC Q93XC0;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)
DE Bax inhibitor 1 (Bax inhibitor-like protein).
GN B1-1 OR B11.
OS Brassica napus (Rape), and
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotsids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708, 3712;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-B.napus; STRAIN=CV. WESTAR; TISSUE=LEAF;
RA Belduc N., Brisson L.;
RT "Characterization of Bax inhibitor 1 from Brassica napus.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-B.oleracea;
RA Coupe S.A., Sinclair B.K., Watson L.M., Bucknell T.T., Eason J.R.;
RT "The isolation and characterization of broccoli homologs to
RT Arabidopsis PCD genes, LSD1 and B1: their role during cell death and
RT senescence.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF310101.1; -
DR EMBL; AF453320; AAL50979.1; -
DR InterPro; IPR002199; Bax_inhbt1.
DR InterPro; IPR001064; Crystallin.
DR Pfam; PF01027; UPF0005; 1.
DR PROSITE; PS01243; B11; UNKNOWN 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN 1.
SQ SEQUENCE 247 AA; 27526 MW; F5A5B5E9F6D4E8DB CRC64;

Query Match 79.4%; Score 1010.5; DB 10; Length 247;
Best Local Similarity 75.4%; Pred. No. 4.5e-81;
Matches 187; Conservative 35; Mismatches 25; Indels 1; Gaps 1;

QY 1 MEGTSPFDSQSASRNWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHL 60
Db 1 MDSFSPFDSQSGRS-WSYDSLKNLRQISPSVQNLKRVYLTLCALVASAFAYLHL 59
QY 61 WNIGGLTTMACGMWMLLSAPPYQOEKRVALLMAALFEGASIGPLIELGNFDPSTV 120
Db 60 WNIGGLTTTACGTMWLLSCPPYQOEKRLSLFLSAVLEGASVGLIKVAVDFPSIL 119
QY 121 FGAFVGCVAVFCFSAAMARRRYLYLGLSSGVSLFLFWLHFASSIFGGSMAVFKFE 180
Db 120 ITAFVGTAFICFSGAAMLARREYLYLGLSSGVSLFLFWLHFASSIFGGSMAVFKFE 179
QY 181 LYFGLLVFVGIVFTQETIEIKAHGDMYVVKHALTFTDFGAVFVRILIMLKNASEK 240
Db 180 LYFGLLVFVGIVFTQETIEIKAHGDMYVVKHALTFTDFGAVFVRILIMLKNASEK 239
QY 241 EKKKKRRN 248
Db 240 EKKKKRRN 245

RESULT 4
Q93XL2 PRELIMINARY; PRT; 247 AA.
AC Q93XL2;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)
DE Bax inhibitor 1.
GN B1-1.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.

```

```

Db 240 DKKKKRRN 247

RESULT 3
Q8W196 PRELIMINARY; PRT; 246 AA.
AC Q8W196;
DT 01-MAR-2002 (TREMELrel. 20, Created)
DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)
DE Bax inhibitor-like protein.
GN B12.
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotsids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
RN [1]
RP SEQUENCE FROM N.A.
RA Coupe S.A., Sinclair B.K., Watson L.M., Bucknell T.T., Eason J.R.;
RT "The isolation and characterization of broccoli homologs to
RT Arabidopsis PCD genes, LSD1 and B1: their role during cell death and
RT senescence.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF453321; AAL50980.1; -
DR InterPro; IPR002199; Bax_inhbt1.
DR InterPro; IPR001064; Crystallin.
DR Pfam; PF01027; UPF0005; 1.
DR PROSITE; PS01243; B11; UNKNOWN 1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN 1.
SQ SEQUENCE 246 AA; 27375 MW; EBD0A01421B2DA2E CRC64;

Query Match 78.8%; Score 1002.5; DB 10; Length 246;
Best Local Similarity 76.0%; Pred. No. 2.2e-80;
Matches 187; Conservative 33; Mismatches 25; Indels 1; Gaps 1;

QY 1 MEGTSPFDSQSASRNWSYDSLKNFRQISPLVQTHLKQVYLTLCCALVASAAGAYLHL 60
Db 1 MDSFSPFDSQSGRS-WSYDSLKNLRQISPSVQNLKRVYLTLCALVASAFAYLHL 59
QY 61 WNIGGLTTMACGMWMLLSAPPYQOEKRVALLMAALFEGASIGPLIELGNFDPSTV 120
Db 60 WNIGGLTTTACGTMWLLSCPPYQOEKRLSLFLSAVLEGASVGLIKVAVDFPSIL 119
QY 121 FGAFVGCVAVFCFSAAMARRRYLYLGLSSGVSLFLFWLHFASSIFGGSMAVFKFE 180
Db 120 ITAFVGTAFICFSGAAMLARREYLYLGLSSGVSLFLFWLHFASSIFGGSMAVFKFE 179
QY 181 LYFGLLVFVGIVFTQETIEIKAHGDMYVVKHALTFTDFGAVFVRILIMLKNASEK 240
Db 180 LYFGLLVFVGIVFTQETIEIKAHGDMYVVKHALTFTDFGAVFVRILIMLKNASEK 239
QY 241 EKKKKRRN 246
Db 240 EKKKKRRN 245

RESULT 4
Q93XL2 PRELIMINARY; PRT; 247 AA.
AC Q93XL2;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMELrel. 20, Last annotation update)
DE Bax inhibitor 1.
GN B1-1.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.

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	RESULT 8	
ID	Q9VIB2 PRELIMINARY; PRT; 305 AA.	
AC	Q9VIB2;	
DT	01-MAY-2000 (TrEMBLrel. 13, Created)	
DDT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	
DDT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)	
DE	CGI287 protein.	
DE	CGI287	
GN	Drosophila melanogaster (Fruit fly).	
OS	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
OCC	Ephydroidea; Drosophilidae; Drosophila.	
OX	NCBI TaxId=7227;	
OR	[1]	
RRP	SEQUENCE FROM N.A.	
RRC	STRAIN=BKRELEV;	
RXC	MEDLINE=20196006; PubMed=10731132;	
RXX	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,	
RAA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,	
RAR	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,	
RAS	Sutton G.C., Morten J.R., Yandell M.D., Zhang Q., Chen L.X.,	
RAT	Brandon R.G., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,	
RAU	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,	
RAV	Abriel J.P., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,	
RAW	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,	
RAZ	Besson K.Y., Benos P.V., Berman B.P., Bhattacharya D., Bolshakov S.,	
RBA	Borkova D., Borchan M.R., Bouck J., Brokstein P., Brotter P.,	
RBB	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,	
RBC	Cherry J.M., Crawley S., Dahlke C., Davenport L.B., Davies P.,	
RBD	de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,	
RBE	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,	
RBF	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,	
RBG	Fowler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,	
RBH	Glodok A., Gong F., Correll J.H., Gu Z., Guan P., Harris M.,	
RBI	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,	
RBJ	Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,	
RBK	Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,	
RBL	Kimmel B.E., Kodira C.D., Kratz C., Kravitz S., Kulp D., Lai Z.,	
RBM	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,	
RBN	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,	
RBO	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,	
RBP	Mount S.M., Moy M., Murphy B., Murphy C., Muzny D.M., Nelson D.L.,	
RBR	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,	
RBS	Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,	
RBT	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,	
RBU	Shue B.C., Siden-Kiamos I., Stimpson M., Skupski M.P., Smith T.,	
RBV	Spier E.C., Spradling A.C., Stapleton M., Strong R., Sun E.,	
RBW	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,	
RBX	Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weisenbach J.,	
RBY	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,	
RBZ	Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao X., Zheng L.,	
RCA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,	
RCB	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;	
RCC	"The genome sequence of Drosophila melanogaster.";	
RCD	Science 287:2185-2195(2000).	
RCE	EMBL: AE003671; AAF54013.1; -	
RCF	FLYBase; FBgn0037506; CGI287.	
RCG	InterPro; IPR002199; Bax_inhbrl.	
RCH	Pfam; PF01027; UPF0005; I.	
RCI	SEQUENCE 305 AA; 32546 MW; 0F25177F36CA9D CRC64;	
QC	Query Match 15.1%; Score 192; DB 5; Length 305;	
QD	Best local similarity 25.7%; Pred. No. 4,6e-05;	
QE	Matches 61; Conservative 49; Mismatches 87; Indels 40; Gaps	
QF	36 HLKQVYLTLCLVASAGAY-----LHLWNIGLLTTWACM-----GSVMYLSAPP 84	
QG	85 HATVAIFGASCVTGAFAVFQTSDAMALTRSGWASLVTLGLVWLSSIAQGLEYP 144	
QH	85 YOQRKVALLMAALFEIASIGLTIELGINFDPSIVFGAFVGCAWFVCFSAAAMLARR 144	


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Db 145 GFGAKQLAWLHVCAVL-GAVLAPMCLLG-----GPILTKALLYTSGIVGALSTVAACAPSE 199
Qy 145 EYLYGLGLSSGVSLFF-----WLHFASIFGSGMAVFKFELYFGLLVFVGYIVFDQ 197
Db 200 KFLHMGGLPLAIGLVFVPASSLASWMLPPTTAVGAG---LASMSLYGGLILFSGFLLYDTQ 256
Qy 198 EIEKAHLGDM-----DYVGHALTFTDFGAVFVRILIMLNKASEKEKKKRN 248
Db 257 RIVKSAELYPOYSKFPYDPINHALAIYDNLNIFIRIAILAGD-----QKRKN 305

RESULT 9
Q87824 PRELIMINARY; PRT; 365 AA.
ID Q87824
AC Q87824
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE AT14090p.
GN CG1287.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champagne M., Chavez C., Dorsett V., Dresnek D., Farfan D., Friese E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY075204; AAL68072.1; -.
SQ SEQUENCE 365 AA; 39108 MW; 676C61176F923745 CRC64;

Query Match 15.1%; Score 192; DB 5; Length 365;
Best Local Similarity 25.7%; Pred. No. 5.6e-09;
Matches 61; Conservative 49; Mismatches 87; Indels 40; Gaps 8;

Qy 36 HLKQVYLTLCALVASAGY-----LHILNIGLLTTWACM-----GSMVWLLSAPP 84
Db 145 HATYAFGASCGVTAASAVFQSDAMMALTRSGWVASLVTGLVMSLSIAQGLGYQP 204
Qy 85 YOEQRVALLMAALFEGASIGPLIELGINFDPISIVFGAFVGCFAVFGCFSAAAMLARR 144
Db 205 GFGAKQLAWLHVCAVL-GAVLAPMCLLG---GPILTKALLYTSGIVGALSTVAACAPSE 259
Qy 145 EYLYGLGLSSGVSLFF-----WLHFASIFGSGMAVFKFELYFGLLVFVGYIVFDQ 197
Db 260 KFLHMGGLPLAIGLVFVPASSLASWMLPPTTAVGAG---LASMSLYGGLILFSGFLLYDTQ 316
Qy 198 EIEKAHLGDM-----DYVGHALTFTDFGAVFVRILIMLNKASEKEKKKRN 248
Db 317 RIVKSAELYPOYSKFPYDPINHALAIYDNLNIFIRIAILAGD-----QKRKN 365

RESULT 10
Q8ZQ61 PRELIMINARY; PRT; 219 AA.
ID Q8ZQ61
AC Q8ZQ61
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative TEGT family carrier/transport protein.
GN YCCA OR STM1085.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella
OX NCBI_TaxID=602;
RN [1]
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RP SEQUENCE FROM N.A.
RC STRAIN=U72 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.B., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT L72."
RL Nature 413:852-856 (2001).
DR EMBL; AE008747; AAL20018.1; -.
DR InterPro; IPR002199; Bax_inhbt1.
DR Pfam; PF01027; UPF0005; 1.
DR PROSITE; PS01243; B11; UNKNOWN_1.
KW Hypothetical protein, Complete Proteome.
SQ SEQUENCE 219 AA; 23313 MW; 9FA28BACE70B8497 CRC64;

Query Match 13.7%; Score 174.5; DB 16; Length 219;
Best Local Similarity 29.6%; Pred. No. 1.1e-07;
Matches 67; Conservative 42; Mismatches 76; Indels 41; Gaps 11;

Qy 27 RQISPLVQTH--LKQVY--LTICCALVASAGYHLHILNIGLLTTWACMGMVWLLSA 82
Db 9 RDRSLLSTHKVLRNTYFLLSLTLASATATATVIMLPSPLGLILTVGMGLMFL---- 65
Qy 83 PPYQ-EQQRVALLMAAL--FEGASIGPLIELGINFDPISIVFG-AFVGCAVFGCFSAAA 138
Db 66 -TYKTANKPVGILLSAFATGTLGVLGILPINAYLSAGMGDVLGALGGTALVFFCCS-AY 123
Qy 139 MLARREYVLGLLSSGVSLF-----WLHFASIFGSGMAVFKFELYFGLL 186
Db 124 VLITRKDMISFLGGMLMAGIVVVLIGMVANIFLQLPALHLAIS-----AVF-----IL 170
Qy 187 VFVGVIVFDTOEIEKAHLGDMYVKHALTLFTDFGAVFVRILIM 232
Db 171 ISSGALLYETSNI--HGGETVYIRATVSLYSLYVLSLSIL 213

RESULT 11
Q9VZ34 PRELIMINARY; PRT; 341 AA.
ID Q9VZ34
AC Q9VZ34;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CG2076 protein.
GN CG2076.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abille J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brattier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pacios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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Best Local Similarity 29.2%; Pred. No. 2.5e-07;
Matches 66; Conservative 42; Mismatches 77; Indels 41; Gaps 11;

QY 27 ROISPLVOTH--LKQVY--LTCCALVASAAGAYLHILWNGIGLTTMACGSMVWLLSA 82
D 9 RORSSLLSTHKVLRNTYFLLSUTLAFSAITATASTVLMPLSPGHLILVGMVGLMFL--- 65
QY 83 PPYQ-EQKREVALMAAL--FEGASIGPLIELGINDPSIVFG-AFVGCVVFGCFSA 138
D 66 -VYKANKVGVLSAFAPFGLGYLIGPLNAYLSAGMGDVIGALGGTALVFPCCS-AY 123
QY 139 MLARREYLYLGLLSSGVSLAF-----WLHPASSIFGSMVAFKELYFGLL 186
D 124 VLTRKMGFLGMLMAGLVVVLIGWNIPLPALHLAIS-----AVF-----IL 170
QY 187 VFYGYVFTFOETIEKAHLGDMYVGHKHALTFTDFGAVFVRILIM 232
D 171 ISSGALYETSNII---HGGETNYIRATVSLVSLYNIFVSLLSIL 213

RESULT 14
Q95309 PRELIMINARY; PRT; 99 AA.
AC Q95309;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE TEGT protein (fragment).
GN TEGT.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=SMALL INTESTINE;
RA Winteroe A.K., Fredholm M., Davies W.;
RT "Evaluation and characterization of a porcine small intestine cDNA
RT library";
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z81159; CAB03546.1; -
DR InterPro; IPR002199; Bax_inhbt1.
DR Pfam; PF01027; UPF0005; 1.
FT NON_TER 99
SQ SEQUENCE 99 AA; 10846 MW; EA009C94B5BE6211 CRC64;

Query Match 12.9%; Score 164; DB 6; Length 99;
Best Local Similarity 36.3%; Pred. No. 4e-07;
Matches 33; Conservative 19; Mismatches 35; Indels 4; Gaps 2;

QY 19 SYDSLKNFRQISPLVQTHLKQVYLTCCALVASAAGAYLHILWNI--GGLLTTMACGSM 76
D 9 NFDALLKFSHTTSTQHLKKVYASFALCNFVAAGAYVHVVTFTIQAGLLSALGLGIM 68
QY 77 WLLSAPPYQ--EQKREVALMAALFEGASI 105
D 69 IWLWATPHSHETQKRLGLLAGFAFLTGVL 99

RESULT 15
Q8XD81 PRELIMINARY; PRT; 219 AA.
AC Q8XD81;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative carrier/transport protein.
DR YCCA OR Z1322 OR ECS1054.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=83334;
RN [1]
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SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoudis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533 (2001).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RMD 0509952;
RX MEDLINE=2115823; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe I.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shingawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22 (2001).
DR EMBL; AE005287; AGS55456.1; -
DR EMBL; AP002554; BAB34477.1; -
DR InterPro; IPR002199; Bax_inhbt1.
DR Pfam; PF01027; UPF0005; 1.
DR PROSITE; PS01243; B11; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 219 AA; 23393 MW; 1AD9F28528D32FFE CRC64;

Query Match 12.4%; Score 157.5; DB 16; Length 219;
Best Local Similarity 26.7%; Pred. No. 3.5e-06;
Matches 64; Conservative 45; Mismatches 80; Indels 51; Gaps 11;

QY 12 SASRNRWSYDSLKNFRQISPLVQTH--LKQVY--LTCCALVASAAGAYLHILWNGIGLL 67
D 6 SSSHRTS-----LLSTHKVLRNTYFLLSUTLAFSAITATASTVLMPLSPGLI 53
QY 68 TTMACGSMVWLLSAPPYQEQKREVALMAAL--FEGASIGPLIELGINDP-PSIVFGAF 124
D 54 LTLVGMVGLMFLTYK--MANKPTGIISAFATGTLGILGILPILNTYLSAGMGDVIAAL 110
QY 125 VGCNVVGCFSAAAMLARREYLYLGLLSSGVSLF-----WLHPASSIFGG 172
D 111 GGTALVFPCCS-AYVLTTRKMGFLGMLMAGIVVVLIGWNIPLPALHLAIS----- 165
QY 173 SNAVFKELYFGLLVFGVYVFDTOETIEKAHLGDMYVGHKHALTFTDFGAVFVRILIM 232
D 166 --AVF-----ILISSGAILPETSNI---HGGETNYIRATVSLVSLYNIFVSLLSIL 213

Search completed: May 25, 2003, 12:22:52
Job time : 61 secs
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